GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 04:57:07 ; Search time 534 Seconds
(without alignments)
9275.219 Million cell updates/sec

Title: US-10-024-444B-1
Perfect score: 977
Sequence: 1 gcaactaaaaaaacacatca.....ttccacgctctagggaagga 977

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3340653 seqs, 2534783454 residues

Word size : 20

Total number of hits satisfying chosen parameters: 200

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	977	100.0	977	15	US-10-024-444B-1	Sequence 1, Appli
2	720	73.7	1033	15	US-10-017-161-635	Sequence 635, App
3	120	12.3	951	9	US-09-886-055-198	Sequence 198, App
4	120	12.3	951	10	US-09-804-291-198	Sequence 198, App
5	120	12.3	951	13	US-10-343-650A-513	Sequence 513, App
6	120	12.3	951	15	US-10-220-382-39	Sequence 39, Appl
7	120	12.3	951	16	US-10-300-846-25	Sequence 25, Appl
8	120	12.3	1008	10	US-09-974-591-11	Sequence 11, Appl
9	120	12.3	1008	10	US-09-974-591-13	Sequence 13, Appl
10	120	12.3	1008	10	US-09-777-789-10	Sequence 10, Appl
11	120	12.3	1008	10	US-09-974-149-11	Sequence 11, Appl
12	120	12.3	1008	10	US-09-974-149-13	Sequence 13, Appl
13	120	12.3	1050	10	US-09-777-789-8	Sequence 8, Appli
14	120	12.3	1351	15	US-10-017-161-309	Sequence 309, App
15	120	12.3	1351	16	US-10-292-798-275	Sequence 275, App
16	88	9.0	507	10	US-09-777-789-45	Sequence 45, Appl
17	88	9.0	528	10	US-09-777-789-40	Sequence 40, Appl
18	27	2.8	678	15	US-10-259-430-45	Sequence 45, Appl
19	27	2.8	678	15	US-10-259-423-45	Sequence 45, Appl
20	27	2.8	912	16	US-10-300-846-15	Sequence 15, Appl
21	26	2.7	26	15	US-10-024-444B-11	Sequence 11, Appl
22	26	2.7	26	16	US-10-024-212-251	Sequence 251, App
23	26	2.7	932	10	US-09-907-218-17	Sequence 17, Appl
24	26	2.7	1337	15	US-10-017-161-835	Sequence 835, App
25	26	2.7	1337	15	US-10-017-161-843	Sequence 843, App
26	26	2.7	1337	16	US-10-292-798-717	Sequence 717, App
27	25	2.6	950	15	US-10-023-597-113	Sequence 113, App
28	25	2.6	1113	13	US-10-027-632-101286	Sequence 101286,
29	25	2.6	1113	16	US-10-027-632-101286	Sequence 101286,
30	25	2.6	1250	15	US-10-017-161-987	Sequence 987, App
31	25	2.6	1250	16	US-10-292-798-843	Sequence 843, App
32	23	2.4	931	15	US-10-017-161-1301	Sequence 1301, Ap
33	23	2.4	931	16	US-10-292-798-1069	Sequence 1069, Ap
34	23	2.4	939	15	US-10-272-417-3	Sequence 3, Appli
35	23	2.4	939	16	US-10-407-079-71	Sequence 71, Appl
36	23	2.4	945	15	US-10-023-597-95	Sequence 95, Appl
37	23	2.4	945	16	US-10-300-846-13	Sequence 13, Appl
38	23	2.4	951	9	US-09-886-055-134	Sequence 134, App
39	23	2.4	951	10	US-09-804-291-134	Sequence 134, App
40	23	2.4	951	13	US-10-343-650A-283	Sequence 283, App
41	23	2.4	951	16	US-10-387-629-21	Sequence 21, Appl
42	23	2.4	962	15	US-10-023-597-115	Sequence 115, App
43	23	2.4	963	15	US-10-023-597-23	Sequence 23, Appl
44	23	2.4	971	13	US-10-433-581-21	Sequence 21, Appl
45	23	2.4	980	15	US-10-025-806-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-10-024-444B-1
; Sequence 1, Application US/10024444B
; Publication No. US20030165858A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Smithson, Glennda
; APPLICANT: Stone, David
; APPLICANT: Bin-Yang, Ruey
; APPLICANT: Conley, Pamela B.
; APPLICANT: Hart, Matthew
; APPLICANT: Tomlinson, James E.
; APPLICANT: Topper, James N.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Casman, Stacie J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Shlomit, Edinger R.
; TITLE OF INVENTION: No. US20030165858A1el GPCR-Like Proteins and Nucleic Acids Encod
; TITLE OF INVENTION: Same
; FILE REFERENCE: 21402-224 AG
; CURRENT APPLICATION NUMBER: US/10/024,444B
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/256635
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Human
US-10-024-444B-1

Query Match 100.0%; Score 977; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GGTGGGGATTCTGAATGACAGTGGGTCTCCTGAACTGCTCTATGCTACATTTACAATCCT 120
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Qy        181 GCTCCACATGCCCATGTACCTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCAC 240
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Qy        241 ATCTGTTGTCACTCCCAAGGCCTTGGCGGACTTTCTGCGCAGAGAAAACACTATCTCCTT 300
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Db        241 ATCTGTTGTCACTCCCAAGGCCTTGGCGGACTTTCTGCGCAGAGAAAACACTATCTCCTT 300

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Db        301 TGGAGGCTGTGCACTTCAGATGTTCCTGGCACTGACAATGGGTAGCGCTGAGGACCTCCT 360

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Db        361 ACTGGCCTTCATGGCCTATGACAGGTATGTGGCCATTTGTCATCCTCTGAAATACATGAC 420

Qy        421 CCTCATGAGCCCAAGAGTCTGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCT 480
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Db        421 CCTCATGAGCCCAAGAGTCTGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCT 480

Qy        481 GATTGCTATAGGACATACCATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAAT 540
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Qy        601 GTATGAGCTTATAATATACGTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCAT 660
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Db        661 TGTGGCCTCCTACACACTAGTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAG 720

Qy        721 GAAGAAAGCCCTTGTCACCTGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGC 780
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Db        721 GAAGAAAGCCCTTGTCACCTGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGC 780

Qy        781 TGCCACATTCATGTATGTCTTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCAT 840
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Db        781 TGCCACATTCATGTATGTCTTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCAT 840

Qy        841 CTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAA 900
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Db        841 CTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAA 900

Qy        901 TAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTC 960

Qy        961 CACGCTCTAGGGAAGGA 977
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Db        961 CACGCTCTAGGGAAGGA 977
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RESULT 2
US-10-017-161-635
; Sequence 635, Application US/10017161
; Publication No. US20030143668A1

; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 635
; LENGTH: 1033
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1033)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(833)
US-10-017-161-635

Query Match 73.7%; Score 720; DB 15; Length 1033;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy        137 ACCAGCAATGGTCTGCTGCTCCTGGCCATCACCATAGAAGCCCGGCTCCACATGCCCATG 196
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Db          1 ACCAGCAATGGTCTGCTGCTCCTGGCCATCACCATAGAAGCCCGGCTCCACATGCCCATG 60

Qy        197 TACCTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCACATCTGTTGTCACTCCC 256
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Db         61 TACCTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCACATCTGTTGTCACTCCC 120

Qy        257 AAGGCCTTGGCGGACTTTCTGCGCAGAGAAAACACTATCTCCTTTGGAGGCTGTGCACTT 316
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Db        121 AAGGCCTT-GCGGACTTTCTGCGCAGAGAAAACACTATCTCCTTTGGAGGCTGTGCACTT 179

Qy        317 CAGATGTTCCTGGCACTGACAATGGGTAGCGCTGAGGACCTCCTACTGGCCTTCATGGCC 376
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Qy        377 TATGACAGGTATGTGGCCATTTGTCATCCTCTGAAATACATGACCCTCATGAGCCCAAGA 436
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Qy        437 GTCTGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTGCTATAGGACAT 496
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Db        300 GTCTGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTGCTATAGGACAT 359

Qy        497 ACCATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAATCAGGCATCTGCTCTGT 556
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Db        360 ACCATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAATCAGGCATCTGCTCTGT 419

Qy        557 GAGATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATGAGCTTATAATA 616
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Db        420 GAGATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATGAGCTTATAATA 479

Qy        617 TACGTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACA 676
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Db        480 TACGTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACA 539

Qy        677 CTAGTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTC 736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CTAGTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTC 599

Qy        737 ACCTGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGCTGCCACATTCATGTAT 796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 ACCTGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGCTGCCACATTCATGTAT 659
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Qy        797 GTCTTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCATCTCTGTTTTCTACACA 856
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Db        660 GTCTTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCATCTCTGTTTTCTACACA 719

Qy        857 ATTGTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGG 916
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Db        720 ATTGTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGG 779

Qy        917 GCCTTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTCCACGCTCTAGGGAAGG 976
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Qy        977 A 977
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Db        840 A 840
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RESULT 3
US-09-886-055-198
; Sequence 198, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 198
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-886-055-198

Query Match 12.3%; Score 120; DB 9; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
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Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926
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RESULT 4
US-09-804-291-198
; Sequence 198, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 198
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-291-198

Query Match 12.3%; Score 120; DB 10; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926
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RESULT 5
US-10-343-650A-513
; Sequence 513, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(951)
US-10-343-650A-513

Query Match 12.3%; Score 120; DB 13; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
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Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926
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RESULT 6
US-10-220-382-39
; Sequence 39, Application US/10220382
; Publication No. US20030119111A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti

```
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  PATTERSON, Chandra
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  SHIH, Leo L.
;  APPLICANT:  TRIBOULEY, Catherine
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  YANG, Junming
;  APPLICANT:  HARLAND, Lee
;  APPLICANT:  WALSH, Roderick T.
;  APPLICANT:  LO, Terence P.
;  APPLICANT:  BOROWSKY, Mark L.
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: PI-0044 PCT
;  CURRENT APPLICATION NUMBER: US/10/220,382
;  CURRENT FILING DATE:  2001-03-01
;  PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
;  PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PERL Program
; SEQ ID NO 39
;   LENGTH: 951
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030119111A1 7472446CB1
US-10-220-382-39

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  Best Local Similarity   100.0%;  Pred. No. 2.2e-51;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 7
US-10-300-846-25
; Sequence 25, Application US/10300846
; Publication No. US20030207337A1
; GENERAL INFORMATION:
;  APPLICANT: HAN, YI
;  APPLICANT:  ZOZULYA, SERGEY
;  APPLICANT:  ECHEVERRI, FERNANDO
;  APPLICANT:  WANG, KUN
;  TITLE OF INVENTION: OLFACTORY RECEPTORS FOR ISOVALERIC ACID AND RELATED
;  TITLE OF INVENTION:  MALODORANTS AND USE THEREOF IN ASSAYS FOR
;  TITLE OF INVENTION:  IDENTIFICATION OF BLOCKERS OF MALODOR
;  FILE REFERENCE: 078003-0291924
;  CURRENT APPLICATION NUMBER: US/10/300,846
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: 60/348,371
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: 09/809,291
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: 60/341,872
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 951
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-300-846-25

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  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
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RESULT 8
US-09-974-591-11
; Sequence 11, Application US/09974591
; Publication No. US20030059830A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook II, John P
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spytek, Kimberly A
;  TITLE OF INVENTION: No. US20030059830A1el Single Nucleotide Polymorphisms for Olfactor
;  TITLE OF INVENTION:  Receptor-like Polypeptides and Nucleic Acids Encoding
;  TITLE OF INVENTION:  the Same
;  FILE REFERENCE: 15966-654 CIP
;  CURRENT APPLICATION NUMBER: US/09/974,591
;  CURRENT FILING DATE:  2001-10-09
;  PRIOR APPLICATION NUMBER: 60/245,292
;  PRIOR FILING DATE: 2000-11-02
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 1008
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (27)..(998)
US-09-974-591-11

  Query Match             12.3%;  Score 120;  DB 10;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-51;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
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Db        917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976


RESULT 9
US-09-974-591-13
; Sequence 13, Application US/09974591
; Publication No. US20030059830A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook II, John P
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spytek, Kimberly A
;  TITLE OF INVENTION: No. US20030059830A1el Single Nucleotide Polymorphisms for Olfactor
;  TITLE OF INVENTION:  Receptor-like Polypeptides and Nucleic Acids Encoding
;  TITLE OF INVENTION:  the Same
;  FILE REFERENCE: 15966-654 CIP
;  CURRENT APPLICATION NUMBER: US/09/974,591
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; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/245,292
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(998)
US-09-974-591-13

Query Match 12.3%; Score 120; DB 10; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Db 857 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 916

Qy 886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
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Db 917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976

RESULT 10
US-09-777-789-10
; Sequence 10, Application US/09777789
; Publication No. US20030087815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-654
; CURRENT APPLICATION NUMBER: US/09/777,789
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/180,646
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-789-10

Query Match 12.3%; Score 120; DB 10; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Qy 886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
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Db 917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976

RESULT 11
US-09-974-149-11
; Sequence 11, Application US/09974149
; Publication No. US20030175705A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Bader, Joel S
; APPLICANT: Bansal, Aruna
; TITLE OF INVENTION: Methods of Use for No. US20030175705A1el Single Nucleotide
; TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
; TITLE OF INVENTION: and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-654UB
; CURRENT APPLICATION NUMBER: US/09/974,149
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/323,755
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(998)
US-09-974-149-11

Query Match 12.3%; Score 120; DB 10; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Db 857 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 916

Qy 886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
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Db 917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976

RESULT 12
US-09-974-149-13
; Sequence 13, Application US/09974149
; Publication No. US20030175705A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Bader, Joel S
; APPLICANT: Bansal, Aruna
; TITLE OF INVENTION: Methods of Use for No. US20030175705A1el Single Nucleotide
; TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
; TITLE OF INVENTION: and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-654UB
; CURRENT APPLICATION NUMBER: US/09/974,149
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/323,755
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (27)..(998)
US-09-974-149-13

Query Match 12.3%; Score 120; DB 10; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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RESULT 13
US-09-777-789-8
; Sequence 8, Application US/09777789
; Publication No. US20030087815A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru et al.
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-654
;  CURRENT APPLICATION NUMBER: US/09/777,789
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: 60/180,646
;  PRIOR FILING DATE: 2000-02-07
;  NUMBER OF SEQ ID NOS: 101
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 1050
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-777-789-8

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RESULT 14
US-10-017-161-309
; Sequence 309, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 084335/0152
;  CURRENT APPLICATION NUMBER: US/10/017,161
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: JP 2001/246789
;  PRIOR FILING DATE: 2001-06-18
;  NUMBER OF SEQ ID NOS: 2430
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 309
;   LENGTH: 1351
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: source
;   LOCATION: (1)..(1351)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (201)..(1151)
US-10-017-161-309

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RESULT 15
US-10-292-798-275
; Sequence 275, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 084335/166
;  CURRENT APPLICATION NUMBER: US/10/292,798
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: 10/017,161
;  PRIOR FILING DATE: 2001-12-18
;  PRIOR APPLICATION NUMBER: JP 2001-246789
;  PRIOR FILING DATE: 2001-06-18
;  NUMBER OF SEQ ID NOS: 2070
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 275
;   LENGTH: 1351
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   LOCATION: source
;   FEATURE:
;   LOCATION: (1)..(1351)
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;   NAME/KEY: CDS
;   LOCATION: (201)..(1151)
US-10-292-798-275

  Query Match             12.3%;  Score 120;  DB 16;  Length 1351;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-51;
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Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
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OM protein - protein search, using sw model

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(without alignments)
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Perfect score: 316
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1351062 seqs, 321799191 residues

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Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	316	100.0	316	14	US-10-024-444B-2	Sequence 2, Appli
2	210	66.5	210	14	US-10-017-161-636	Sequence 636, App
3	57	18.0	316	9	US-09-886-055-197	Sequence 197, App
4	57	18.0	316	10	US-09-777-789-9	Sequence 9, Appli
5	57	18.0	316	10	US-09-804-291-197	Sequence 197, App
6	57	18.0	316	11	US-09-912-976-53	Sequence 53, Appl
7	57	18.0	316	11	US-09-965-422-58	Sequence 58, Appl
8	57	18.0	316	12	US-10-343-650A-514	Sequence 514, App
9	57	18.0	316	14	US-10-220-382-18	Sequence 18, Appl
10	57	18.0	316	14	US-10-017-161-310	Sequence 310, App
11	57	18.0	316	14	US-10-024-444B-3	Sequence 3, Appli
12	57	18.0	316	15	US-10-300-846-26	Sequence 26, Appl
13	57	18.0	316	15	US-10-292-798-276	Sequence 276, App
14	57	18.0	324	10	US-09-974-591-12	Sequence 12, Appl
15	57	18.0	324	10	US-09-974-591-14	Sequence 14, Appl
16	57	18.0	324	10	US-09-777-789-11	Sequence 11, Appl
17	57	18.0	324	10	US-09-974-149-12	Sequence 12, Appl
18	57	18.0	324	10	US-09-974-149-14	Sequence 14, Appl
19	43	13.6	316	11	US-09-912-976-50	Sequence 50, Appl
20	43	13.6	316	11	US-09-912-976-51	Sequence 51, Appl
21	43	13.6	316	11	US-09-965-422-60	Sequence 60, Appl
22	43	13.6	316	14	US-10-024-444B-5	Sequence 5, Appli
23	43	13.6	316	14	US-10-024-444B-6	Sequence 6, Appli
24	29	9.2	316	10	US-09-795-271-51	Sequence 51, Appl
25	29	9.2	316	14	US-10-024-444B-4	Sequence 4, Appli
26	28	8.9	316	10	US-09-777-789-41	Sequence 41, Appl
27	28	8.9	316	10	US-09-777-789-42	Sequence 42, Appl
28	28	8.9	316	10	US-09-777-789-46	Sequence 46, Appl
29	28	8.9	316	10	US-09-777-789-47	Sequence 47, Appl
30	28	8.9	316	10	US-09-795-271-48	Sequence 48, Appl
31	28	8.9	316	11	US-09-912-976-52	Sequence 52, Appl
32	28	8.9	316	11	US-09-965-422-56	Sequence 56, Appl
33	28	8.9	316	14	US-10-024-444B-7	Sequence 7, Appli
34	28	8.9	316	15	US-10-005-041A-104	Sequence 104, App
35	23	7.3	319	10	US-09-795-271-50	Sequence 50, Appl
36	23	7.3	319	11	US-09-965-422-57	Sequence 57, Appl
37	17	5.4	315	10	US-09-795-271-49	Sequence 49, Appl
38	17	5.4	315	11	US-09-965-422-59	Sequence 59, Appl
39	17	5.4	315	11	US-09-981-566A-71	Sequence 71, Appl
40	17	5.4	315	15	US-10-005-041A-105	Sequence 105, App
41	15	4.7	316	14	US-10-023-597-68	Sequence 68, Appl
42	14	4.4	317	9	US-09-886-055-201	Sequence 201, App
43	14	4.4	317	10	US-09-804-291-201	Sequence 201, App
44	14	4.4	317	10	US-09-907-218-2	Sequence 2, Appli
45	14	4.4	317	10	US-09-907-218-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-024-444B-2
; Sequence 2, Application US/10024444B
; Publication No. US20030165858A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Smithson, Glennda
; APPLICANT: Stone, David
; APPLICANT: Bin-Yang, Ruey
; APPLICANT: Conley, Pamela B.
; APPLICANT: Hart, Matthew
; APPLICANT: Tomlinson, James E.
; APPLICANT: Topper, James N.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Casman, Stacie J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Shlomit, Edinger R.
; TITLE OF INVENTION: No. US20030165858A1el GPCR-Like Proteins and Nucleic Acids Encod
; TITLE OF INVENTION: Same
; FILE REFERENCE: 21402-224 AG
; CURRENT APPLICATION NUMBER: US/10/024,444B
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/256635
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Human
US-10-024-444B-2

Query Match 100.0%; Score 316; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.6e-284;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MELRNSTLGSGFILVGILNDSGSPELLYATFTILYMLALTSNGLLLLAITIEARLHMPMY 60

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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELRNSTLGSGFILVGILNDSGSPELLYATFTILYMLALTSNGLLLLAITIEARLHMPMY 60

Qy         61 LLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMGSAEDLLLAFMAY 120
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMGSAEDLLLAFMAY 120

Qy        121 DRYVAICHPLKYMTLMSPRVCWIMVATSWILASLIAIGHTMYTMHLPFCVSWEIRHLLCE 180
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRYVAICHPLKYMTLMSPRVCWIMVATSWILASLIAIGHTMYTMHLPFCVSWEIRHLLCE 180

Qy        181 IPPLLKLACADTSRYELIIYVTGVTFLLLPISAIVASYTLVLFTVLRMPSNEGRKKALVT 240
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IPPLLKLACADTSRYELIIYVTGVTFLLLPISAIVASYTLVLFTVLRMPSNEGRKKALVT 240

Qy        241 CSSHLIVVGMFYGAATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEVMRA 300
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CSSHLIVVGMFYGAATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEVMRA 300

Qy        301 LRRVLGKYILLAHSTL 316
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Db        301 LRRVLGKYILLAHSTL 316


RESULT 2
US-10-017-161-636
; Sequence 636, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 084335/0152
;  CURRENT APPLICATION NUMBER: US/10/017,161
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: JP 2001/246789
;  PRIOR FILING DATE: 2001-06-18
;  NUMBER OF SEQ ID NOS: 2430
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 636
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-017-161-636

  Query Match             66.5%;  Score 210;  DB 14;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-186;
  Matches  210;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 MGSAEDLLLAFMAYDRYVAICHPLKYMTLMSPRVCWIMVATSWILASLIAIGHTMYTMHL 166
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSAEDLLLAFMAYDRYVAICHPLKYMTLMSPRVCWIMVATSWILASLIAIGHTMYTMHL 60

Qy        167 PFCVSWEIRHLLCEIPPLLKLACADTSRYELIIYVTGVTFLLLPISAIVASYTLVLFTVL 226
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PFCVSWEIRHLLCEIPPLLKLACADTSRYELIIYVTGVTFLLLPISAIVASYTLVLFTVL 120

Qy        227 RMPSNEGRKKALVTCSSHLIVVGMFYGAATFMYVLPSSFHSPKQDNIISVFYTIVTPALN 286
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RMPSNEGRKKALVTCSSHLIVVGMFYGAATFMYVLPSSFHSPKQDNIISVFYTIVTPALN 180

Qy        287 PLIYSLRNKEVMRALRRVLGKYILLAHSTL 316
                  ||||||||||||||||||||||||||||||
Db        181 PLIYSLRNKEVMRALRRVLGKYILLAHSTL 210


RESULT 3
US-09-886-055-197
; Sequence 197, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
;  APPLICANT: STRYER, LUBERT
;  APPLICANT:  ZOZULYA, SERGEY
;  TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
;  TITLE OF INVENTION:  BIOSENSORS OF CHEMICAL SENSANTS
;  FILE REFERENCE: 078003-0277150
;  CURRENT APPLICATION NUMBER: US/09/886,055
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: 60/213,812
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 522
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 197
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-886-055-197

  Query Match             18.0%;  Score 57;  DB 9;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108


RESULT 4
US-09-777-789-9
; Sequence 9, Application US/09777789
; Publication No. US20030087815A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru et al.
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-654
;  CURRENT APPLICATION NUMBER: US/09/777,789
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: 60/180,646
;  PRIOR FILING DATE: 2000-02-07
;  NUMBER OF SEQ ID NOS: 101
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-777-789-9

  Query Match             18.0%;  Score 57;  DB 10;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108


RESULT 5
US-09-804-291-197
; Sequence 197, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
;  APPLICANT: ZOZULA, SERGEY
;  TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
;  FILE REFERENCE: P 0278005
;  CURRENT APPLICATION NUMBER: US/09/804,291
;  CURRENT FILING DATE:  2001-03-13
;  PRIOR APPLICATION NUMBER: 60/188,914
;  PRIOR FILING DATE: 2000-03-13
;  PRIOR APPLICATION NUMBER: 60/192,033
;  PRIOR FILING DATE: 2000-03-24
;  PRIOR APPLICATION NUMBER: 60/198,474
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/199,335
;  PRIOR FILING DATE: 2000-04-24
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;  PRIOR APPLICATION NUMBER: 60/207,702
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/213,849
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: 60/226,534
;  PRIOR FILING DATE: 2000-08-16
;  PRIOR APPLICATION NUMBER: 60/230,732
;  PRIOR FILING DATE: 2000-09-07
;  PRIOR APPLICATION NUMBER: 60/266,862
;  PRIOR FILING DATE: 2001-02-07
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 197
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-804-291-197

  Query Match             18.0%;  Score 57;  DB 10;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108


RESULT 6
US-09-912-976-53
; Sequence 53, Application US/09912976
; Publication No. US20030212255A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT:  Mezes, Peter
;  APPLICANT:  Burgess, Catherine
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Gerlach, Valerie L
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Mishra, Vishnu
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-070
;  CURRENT APPLICATION NUMBER: US/09/912,976
;  CURRENT FILING DATE:  2001-07-05
;  PRIOR APPLICATION NUMBER: 60/221,336
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/238,333
;  PRIOR FILING DATE: 2000-10-05
;  PRIOR APPLICATION NUMBER: 60/260,675
;  PRIOR FILING DATE: 2001-01-10
;  PRIOR APPLICATION NUMBER: 60/271,025
;  PRIOR FILING DATE: 2001-02-22
;  PRIOR APPLICATION NUMBER: 60/278,164
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: 60/280,876
;  PRIOR FILING DATE: 2001-04-02
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-912-976-53

  Query Match             18.0%;  Score 57;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108


RESULT 7
US-09-965-422-58
; Sequence 58, Application US/09965422
; Publication No. US20030216545A1
; GENERAL INFORMATION:
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Dickson, Kevin
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Li, Li
;  APPLICANT:  Malyankar, Urial M
;  APPLICANT:  Taylor, Sarah
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Tchernev, Velizar T
;  TITLE OF INVENTION: No. US20030216545A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21401-132
;  CURRENT APPLICATION NUMBER: US/09/965,422
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: 60/236,286
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: 60/236,284
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: 60/237,581
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/238,735
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: 60/240,736
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 60/260,019
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,338
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/262,156
;  PRIOR FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: 60/262,498
;  PRIOR FILING DATE: 2001-01-18
;  PRIOR APPLICATION NUMBER: 60/263,133
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,691
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/266,109
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/271,634
;  PRIOR FILING DATE: 2001-02-26
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-965-422-58

  Query Match             18.0%;  Score 57;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108


RESULT 8
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US-10-343-650A-514
; Sequence 514, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 514
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-514

Query Match 18.0%; Score 57; DB 12; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
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Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 9
US-10-220-382-18
; Sequence 18, Application US/10220382
; Publication No. US20030119111A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: YAO, Monique G.
; APPLICANT: SHIH, Leo L.
; APPLICANT: TRIBOULEY, Catherine
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROWSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/10/220,382
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119111A1 7472446CD1
US-10-220-382-18

Query Match 18.0%; Score 57; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 10
US-10-017-161-310
; Sequence 310, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 310
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-310

Query Match 18.0%; Score 57; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 11
US-10-024-444B-3
; Sequence 3, Application US/10024444B
; Publication No. US20030165858A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Smithson, Glennda
; APPLICANT: Stone, David
; APPLICANT: Bin-Yang, Ruey
; APPLICANT: Conley, Pamela B.
; APPLICANT: Hart, Matthew
; APPLICANT: Tomlinson, James E.
; APPLICANT: Topper, James N.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Casman, Stacie J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Shlomit, Edinger R.
; TITLE OF INVENTION: No. US20030165858A1el GPCR-Like Proteins and Nucleic Acids Encodir
; TITLE OF INVENTION: Same
; FILE REFERENCE: 21402-224 AG
; CURRENT APPLICATION NUMBER: US/10/024,444B
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/256635
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 316
; TYPE: PRT
; ORGANISM: human
US-10-024-444B-3

Query Match 18.0%; Score 57; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
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RESULT 12
US-10-300-846-26
; Sequence 26, Application US/10300846
; Publication No. US20030207337A1
; GENERAL INFORMATION:
; APPLICANT: HAN, YI
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ECHEVERRI, FERNANDO
; APPLICANT: WANG, KUN
; TITLE OF INVENTION: OLFACTORY RECEPTORS FOR ISOVALERIC ACID AND RELATED
; TITLE OF INVENTION: MALODORANTS AND USE THEREOF IN ASSAYS FOR
; TITLE OF INVENTION: IDENTIFICATION OF BLOCKERS OF MALODOR
; FILE REFERENCE: 078003-0291924
; CURRENT APPLICATION NUMBER: US/10/300,846
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/348,371
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/809,291
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/341,872
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-846-26

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  Query Match             18.0%;  Score 57;  DB 15;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
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RESULT 13
US-10-292-798-276
; Sequence 276, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 276
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-276

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  Query Match             18.0%;  Score 57;  DB 15;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
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RESULT 14
US-09-974-591-12
; Sequence 12, Application US/09974591
; Publication No. US20030059830A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; TITLE OF INVENTION: No. US20030059830A1el Single Nucleotide Polymorphisms for Olfacto
; TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding
; TITLE OF INVENTION: the Same
; FILE REFERENCE: 15966-654 CIP
; CURRENT APPLICATION NUMBER: US/09/974,591
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/245,292
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-591-12

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  Best Local Similarity   100.0%;  Pred. No. 3.3e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          60 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 116
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RESULT 15
US-09-974-591-14
; Sequence 14, Application US/09974591
; Publication No. US20030059830A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; TITLE OF INVENTION: No. US20030059830A1el Single Nucleotide Polymorphisms for Olfacto
; TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding
; TITLE OF INVENTION: the Same
; FILE REFERENCE: 15966-654 CIP
; CURRENT APPLICATION NUMBER: US/09/974,591
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/245,292
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-591-14

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  Query Match             18.0%;  Score 57;  DB 10;  Length 324;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
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Db          60 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 116
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Search completed: October 5, 2004, 14:36:23
Job time : 131 secs

OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 03:17:06 ; Search time 2511 Seconds
(without alignments)
11619.016 Million cell updates/sec

Title: US-10-024-444B-1
Perfect score: 977
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 20

Total number of hits satisfying chosen parameters: 94

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	121	12.4	710	29	AG031161	AG031161 Pan trogl
	2	89	9.1	663	29	AG090554	AG090554 Pan trogl
	3	84	8.6	566	28	AQ522745	AQ522745 HS_5221_B
	4	43	4.4	843	10	BE897401	BE897401 601437394
c	5	38	3.9	625	28	AZ373068	AZ373068 1M0125N08
c	6	31	3.2	455	28	AZ806221	AZ806221 2M0068E10
	7	31	3.2	528	14	CB174035	CB174035 OR_2o32D0
	8	31	3.2	595	14	CB173529	CB173529 OR_2o28D0
c	9	28	2.9	432	28	AZ323827	AZ323827 1M0045B03
	10	28	2.9	545	28	BH352344	BH352344 CH230-136
c	11	28	2.9	680	28	AZ709687	AZ709687 RPCI-24-8
	12	26	2.7	222	10	BF444685	BF444685 262681 MA
	13	26	2.7	334	10	AW486191	AW486191 71360 MAR
	14	26	2.7	387	28	BZ949576	BZ949576 CH240_380
c	15	26	2.7	451	12	BI399100	BI399100 MI-P-AY1-
	16	26	2.7	461	14	CB173429	CB173429 OR_2o10G0
	17	26	2.7	496	10	AW431124	AW431124 71365 MAR
	18	26	2.7	541	14	CB173558	CB173558 OR_2o30B1
	19	26	2.7	605	28	AZ642411	AZ642411 1M0505L22
c	20	26	2.7	632	28	AZ392351	AZ392351 1M0154L21
	21	26	2.7	968	13	BY716264	BY716264 BY716264
	22	26	2.7	1394	11	AK017036	AK017036 Mus muscu
	23	26	2.7	3063	11	AK016560	AK016560 Mus muscu
c	24	23	2.4	393	29	CE644671	CE644671 tigr-gss-
c	25	23	2.4	456	12	BI274717	BI274717 UI-R-CX0-
	26	23	2.4	504	14	CB174105	CB174105 OR_2o34C0
	27	23	2.4	560	14	CB173336	CB173336 OR_2o16G0
	28	23	2.4	588	14	CB173379	CB173379 OR_2o27H0
	29	23	2.4	605	14	CB174014	CB174014 OR_2o31G0
c	30	23	2.4	634	28	AZ374178	AZ374178 1M0126F17
	31	23	2.4	683	28	AQ931094	AQ931094 RPCI-23-2
c	32	23	2.4	1201	9	AL539244	AL539244 AL539244
	33	22	2.3	318	13	BY674185	BY674185 BY674185
	34	22	2.3	362	13	BY674725	BY674725 BY674725
c	35	22	2.3	406	28	BZ887731	BZ887731 CH240_244
	36	22	2.3	438	28	B06163	B06163 cSRL-76h8-u
c	37	22	2.3	486	28	AQ456128	AQ456128 HS_5095_B
c	38	22	2.3	725	29	AG077338	AG077338 Pan trogl
c	39	22	2.3	808	14	CD656752	CD656752 AGENCOURT
	40	21	2.1	467	14	CB173469	CB173469 OR_2o13F0
	41	21	2.1	493	14	CB173224	CB173224 OR_2o10D0
	42	21	2.1	550	14	CB173653	CB173653 OR_2o22D0
	43	21	2.1	601	14	CB173253	CB173253 OR_2o11C0
	44	21	2.1	626	14	CB172978	CB172978 OR_2o19A0
c	45	21	2.1	627	28	BZ117050	BZ117050 CH230-472

ALIGNMENTS

RESULT 1
AG031161
LOCUS AG031161 710 bp DNA linear GSS 01-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-005A07.F, genomic survey sequence.
ACCESSION AG031161
VERSION AG031161.1 GI:16558034
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 710)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of

clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.

FEATURES Location/Qualifiers
source 1. .710
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-005A07.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 12.4%; Score 121; DB 29; Length 710;
Best Local Similarity 99.1%; Pred. No. 3.2e-52;
Matches 221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        426 TGAGCCCAAGAGTCTGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTG 485
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Db        479 TGAGCCCAAGAGTCTGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTG 538

Qy        486 CTATAGGACATACCATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAATCAGGC 545
              |||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||
Db        539 CTATAGGACATACCATGTACACTATGCACCTCCCTTTCTGCGTGTCCTGCGAAATCAGGC 598

Qy        546 ATCTGCTCTGTGAGATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATG 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATCTGCTCTGTGAGATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATG 658

Qy        606 AGCTTATAATATACGTGACAGGTGTGACTTTCCTCTTGCTCCC 648
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Db        659 AGCTTATAATATACGTGACAGGTGTGACTTTCCTCTTGCTCCC 701
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RESULT 2
AG090554
LOCUS AG090554 663 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-090C09.R, genomic survey sequence.
ACCESSION AG090554
VERSION AG090554.1 GI:16642356
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 663)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.

FEATURES Location/Qualifiers
source 1. .663
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-090C09.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 9.1%; Score 89; DB 29; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.7e-35;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        173 GAAGCCCGGCTCCACATGCCCATGTACCTCCTGCTTGGGCAGCTCTCTCTCATGGACCTC 232
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Db        211 GAAGCCCGGCTCCACATGCCCATGTACCTCCTGCTTGGGCAGCTCTCTCTCATGGACCTC 270

Qy        233 CTGTTCACATCTGTTGTCACTCCCAAGGC 261
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Db        271 CTGTTCACATCTGTTGTCACTCCCAAGGC 299
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RESULT 3
AQ522745
LOCUS AQ522745 566 bp DNA linear GSS 11-MAY-1999
DEFINITION HS_5221_B1_B10_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=797 Col=19 Row=D, genomic survey sequence.
ACCESSION AQ522745
VERSION AQ522745.1 GI:4770252
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 566)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 797 row: D column: 19
Seq primer: T7
Class: BAC ends
High quality sequence stop: 566.

FEATURES Location/Qualifiers
source 1. .566
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=797 Col=19 Row=D"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 8.6%; Score 84; DB 28; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         45 GAAGCGGCTTCATCTTGGTGGGGATTCTGAATGACAGTGGGTCTCCTGAACTGCTCTATG 104
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Db        432 GAAGCGGCTTCATCTTGGTGGGGATTCTGAATGACAGTGGGTCTCCTGAACTGCTCTATG 491

Qy        105 CTACATTTACAATCCTATACATGT 128
              |||||||||||||||||||||||
Db        492 CTACATTTACAATCCTATACATGT 515
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RESULT 4
BE897401
LOCUS BE897401 843 bp mRNA linear EST 20-OCT-2000
DEFINITION 601437394F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922342 5', mRNA sequence.
ACCESSION BE897401
VERSION BE897401.1 GI:10362826
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 843)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9756 row: 1 column: 23
High quality sequence start: 12
High quality sequence stop: 614.

FEATURES Location/Qualifiers
source 1. .843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3922342"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 4.4%; Score 43; DB 10; Length 843;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         634 TTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACA 676
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Db         129 TTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACA 171
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RESULT 5
AZ373068/c
LOCUS AZ373068 625 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0125N08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0125N08 F, genomic survey sequence.
ACCESSION AZ373068
VERSION AZ373068.1 GI:10486768
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 625)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0125 row: N column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 625.

FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0125N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.9%; Score 38; DB 28; Length 625;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         371 ATGGCCTATGACAGGTATGTGGCCATTTGTCATCCTCT 408
               ||||||||||||||||||||||||||||||||||||||
Db         255 ATGGCCTATGACAGGTATGTGGCCATTTGTCATCCTCT 218
```

RESULT 6
AZ806221/c
LOCUS AZ806221 455 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0068E10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

```
            clone UUGC2M0068E10 F, genomic survey sequence.
ACCESSION   AZ806221
VERSION     AZ806221.1  GI:12967032
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0068  row: E  column: 10
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 455.
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0068E10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             3.2%;  Score 31;  DB 28;  Length 455;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        881 CTCATCTACAGCCTGAGGAATAAGGAGGTCA 911
              |||||||||||||||||||||||||||||||
Db        303 CTCATCTACAGCCTGAGGAATAAGGAGGTCA 273


RESULT 7
CB174035
LOCUS       CB174035                528 bp    mRNA    linear   EST 09-OCT-2003
DEFINITION  OR_2o32D01_010529.y1 Adult mouse olfactory epithelium library Mus
            musculus cDNA clone 2o32D01 5', mRNA sequence.
ACCESSION   CB174035
VERSION     CB174035.1  GI:37592664
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   Young,J.M., Shykind,B.M., Lane,R.P., Tonnes-Priddy,L., Ross,J.A.,
            Walker,M., Williams,E.M. and Trask,B.J.
  TITLE     Odorant receptor expressed sequence tags demonstrate olfactory
            expression of over 400 genes, extensive alternate splicing and
            unequal expression levels
  JOURNAL   Genome Biol. 4 (11), R71.1-R71.15 (2003)
COMMENT     Contact: Young JM
            Trask Lab, Division of Human Biology
            Fred Hutchinson Cancer Research Center
            1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
            98109-1024, USA
            Tel: 206 667 1471
            Fax: 206 667 6524
            Email: jayoung@fhcrc.org
            Young gene new name GA_x6K02T2Q125-47640742-47639798
            Young gene old name GA_x5J8B7W3KVV-147900-148844
            Zhang gene name MOR185-4
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .528
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="2o32D01"
                     /tissue_type="Olfactory and respiratory epithelium"
                     /dev_stage="Adult"
                     /clone_lib="Adult mouse olfactory epithelium library"
                     /note="Organ: Olfactory turbinates; Vector:
                     LambdaZAPII-XR; Site_1: EcoRI; Site_2: XhoI; This library
                     was provided by Leslie Vosshall. mRNA was prepared from
                     the olfactory and respiratory epithelium of an adult
                     mouse. Oligo-dT primed cDNA was directionally cloned into
                     Stratagene's lambdaZAPII-XR vector."
ORIGIN

  Query Match             3.2%;  Score 31;  DB 14;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 0.00013;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 CATGGCCTATGACAGGTATGTGGCCATTTGT 400
              |||||||||||||||||||||||||||||||
Db        187 CATGGCCTATGACAGGTATGTGGCCATTTGT 217


RESULT 8
CB173529
LOCUS       CB173529                595 bp    mRNA    linear   EST 09-OCT-2003
DEFINITION  OR_2o28D09_010501.y1 Adult mouse olfactory epithelium library Mus
            musculus cDNA clone 2o28D09 5', mRNA sequence.
ACCESSION   CB173529
VERSION     CB173529.1  GI:37592158
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Young,J.M., Shykind,B.M., Lane,R.P., Tonnes-Priddy,L., Ross,J.A.,
            Walker,M., Williams,E.M. and Trask,B.J.
  TITLE     Odorant receptor expressed sequence tags demonstrate olfactory
            expression of over 400 genes, extensive alternate splicing and
            unequal expression levels
  JOURNAL   Genome Biol. 4 (11), R71.1-R71.15 (2003)
COMMENT     Contact: Young JM
```

Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA 98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org
Young gene new name GA_x6K02T2Q125-47640742-47639798
Young gene old name GA_x5J8B7W3KVV-147900-148844
Zhang gene name MOR185-4
Seq primer: M13 Reverse.

FEATURES Location/Qualifiers
source 1. .595
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2o28D09"
/tissue_type="Olfactory and respiratory epithelium"
/dev_stage="Adult"
/clone_lib="Adult mouse olfactory epithelium library"
/note="Organ: Olfactory turbinates; Vector: LambdaZAPII-XR; Site_1: EcoRI; Site_2: XhoI; This library was provided by Leslie Vosshall. mRNA was prepared from the olfactory and respiratory epithelium of an adult mouse. Oligo-dT primed cDNA was directionally cloned into Stratagene's lambdaZAPII-XR vector."

ORIGIN

Query Match 3.2%; Score 31; DB 14; Length 595;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 CATGGCCTATGACAGGTATGTGGCCATTTGT 400
||||||||||||||||||||||||||||||
Db 386 CATGGCCTATGACAGGTATGTGGCCATTTGT 416

RESULT 9
AZ323827/c
LOCUS AZ323827 432 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0045B03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0045B03 R, genomic survey sequence.
ACCESSION AZ323827
VERSION AZ323827.1 GI:10378931
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 432)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: B column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 432.

FEATURES Location/Qualifiers
source 1. .432
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0045B03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 2.9%; Score 28; DB 28; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 369 TCATGGCCTATGACAGGTATGTGGCCAT 396
||||||||||||||||||||||||||||
Db 250 TCATGGCCTATGACAGGTATGTGGCCAT 223

RESULT 10
BH352344
LOCUS BH352344 545 bp DNA linear GSS 03-DEC-2001
DEFINITION CH230-136E3.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-136E3, genomic survey sequence.
ACCESSION BH352344
VERSION BH352344.1 GI:17283078
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 545)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment
JOURNAL Unpublished (1999)
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 136 row: E column: 3
Seq primer: T7
Class: BAC ends.

FEATURES Location/Qualifiers

```
     source          1. .545
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-136E3"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 1"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN

  Query Match             2.9%;  Score 28;  DB 28;  Length 545;
  Best Local Similarity   100.0%;  Pred. No. 0.005;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        369 TCATGGCCTATGACAGGTATGTGGCCAT 396
              ||||||||||||||||||||||||||||
Db        212 TCATGGCCTATGACAGGTATGTGGCCAT 239


RESULT 11
AZ709687/c
LOCUS       AZ709687                680 bp    DNA     linear   GSS 24-JAN-2001
DEFINITION  RPCI-24-82P2.TJ RPCI-24 Mus musculus genomic clone RPCI-24-82P2,
            genomic survey sequence.
ACCESSION   AZ709687
VERSION     AZ709687.1  GI:12440500
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-24-82P2.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 82  row: P  column: 2
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-82P2"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /clone_lib="RPCI-24"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was  cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI  partially digested male C57BL/6J
                     DNA."
ORIGIN

  Query Match             2.9%;  Score 28;  DB 28;  Length 680;
  Best Local Similarity   100.0%;  Pred. No. 0.0052;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 CATGGCCTATGACAGGTATGTGGCCATT 397
              |||||||||||||||||||||||||||||
Db        463 CATGGCCTATGACAGGTATGTGGCCATT 436


RESULT 12
BF444685
LOCUS       BF444685                222 bp    mRNA    linear   EST 01-DEC-2000
DEFINITION  262681 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BF444685
VERSION     BF444685.1  GI:11504777
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 222)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 98  row: G  column: 8
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .222
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 2PIG"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
ORIGIN

  Query Match             2.7%;  Score 26;  DB 10;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 0.046;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        881 CTCATCTACAGCCTGAGGAATAAGGA 906
              ||||||||||||||||||||||||||
Db        157 CTCATCTACAGCCTGAGGAATAAGGA 182


RESULT 13
AW486191
LOCUS       AW486191                334 bp    mRNA    linear   EST 09-JUL-2000
DEFINITION  71360 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   AW486191
VERSION     AW486191.1  GI:7056297
KEYWORDS    EST.
```

```
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 30  row: D  column: 6
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 1PIG"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
ORIGIN

  Query Match             2.7%;  Score 26;  DB 10;  Length 334;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        881 CTCATCTACAGCCTGAGGAATAAGGA 906
              ||||||||||||||||||||||||||
Db         90 CTCATCTACAGCCTGAGGAATAAGGA 115


RESULT 14
BZ949576
LOCUS       BZ949576                387 bp    DNA     linear   GSS 13-JUN-2003
DEFINITION  CH240_38O9.TV CHORI-240 Bos taurus genomic clone CH240_38O9,
            genomic survey sequence.
ACCESSION   BZ949576
VERSION     BZ949576.1  GI:31734881
KEYWORDS    GSS.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 387)
  AUTHORS   Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P.,
            Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L.,
            Womack,J.E., de Jong,P.J. and Lewin,H.A.
  TITLE     A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
            Genome Sequence
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Harris Lewin
            Department of Animal Sciences
            University of Illinois at Urbana Champaign
            1201 W. Gregory Dr., Urbana, IL 61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Clones are derived from the bovine BAC library CHORI-240
            (http://www.chori.org/bacpac/bovine240.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/ordering_information.htm). This work
            was undertaken as part of the International Bovine BAC Mapping
            Consortium (IBBMC) by by University of Illinois at Urbana
            Champaign, USA with funds provided by grant No. AG202-34480-11828
            from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock
            Genome Sequencing Initiative)
            Plate: 38  row: O  column: 9
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="breed: Hereford"
                     /db_xref="taxon:9913"
                     /clone="CH240_38O9"
                     /sex="Male"
                     /cell_type="Blood"
                     /clone_lib="CHORI-240"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
                     library (Male) produced by Pieter de Jong"
ORIGIN

  Query Match             2.7%;  Score 26;  DB 28;  Length 387;
  Best Local Similarity   100.0%;  Pred. No. 0.053;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        884 ATCTACAGCCTGAGGAATAAGGAGGT 909
              ||||||||||||||||||||||||||
Db        222 ATCTACAGCCTGAGGAATAAGGAGGT 247


RESULT 15
BI399100/c
LOCUS       BI399100                451 bp    mRNA    linear   EST 14-AUG-2001
DEFINITION  MI-P-AY1-nrk-c-11-0-UI.s1 MI-P-AY1 Sus scrofa cDNA clone
            MI-P-AY1-nrk-c-11-0-UI 3', mRNA sequence.
ACCESSION   BI399100
VERSION     BI399100.1  GI:15178161
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            normalized placenta library cDNA Library Preparation: M.B. Soares
            Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
```

of Iowa Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .451
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-AY1-nrk-c-11-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="MI-P-AY1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AY1 library is normalized library derived from the MI-P-AY0 library, ultimately derived from placenta tissue. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG_TISSUE=placenta
TAG_LIB=MI-P-AY1
TAG_SEQ=ATTGG"

ORIGIN

Query Match 2.7%; Score 26; DB 12; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 881 CTCATCTACAGCCTGAGGAATAAGGA 906
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Db 61 CTCATCTACAGCCTGAGGAATAAGGA 36

Search completed: October 6, 2004, 05:39:08
Job time : 2521 secs

OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 01:54:16 ; Search time 3864 Seconds
(without alignments)
10959.147 Million cell updates/sec

Title: US-10-024-444B-1
Perfect score: 977
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 20

Total number of hits satisfying chosen parameters: 679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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8: gb_pl:*
9: gb_pr:*
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12: gb_sy:*
13: gb_un:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		977	100.0	977	6	AX686711	AX686711 Sequence
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3		856	87.6	1350	9	AB065539	AB065539 Homo sapi
4	c	856	87.6	208430	2	AC027641	AC027641 Homo sapi
5		827	84.6	947	6	AX241682	AX241682 Sequence
6		605	61.9	649	9	AF399487	AF399487 Homo sapi
7		120	12.3	948	6	AX241679	AX241679 Sequence
8		120	12.3	951	6	AX244613	AX244613 Sequence
9		120	12.3	951	6	AX448455	AX448455 Sequence
10		120	12.3	951	6	BD144532	BD144532 Novel G-p
11		120	12.3	1008	6	AX210250	AX210250 Sequence
12		120	12.3	1008	6	AX551018	AX551018 Sequence
13		120	12.3	1008	6	AX551020	AX551020 Sequence
14		120	12.3	1050	6	AX210248	AX210248 Sequence
15		120	12.3	1351	6	AX646083	AX646083 Sequence
16		120	12.3	1351	9	AB065823	AB065823 Homo sapi
17	c	120	12.3	171660	2	AC017103	AC017103 Homo sapi
18		120	12.3	173611	9	AC087280	AC087280 Homo sapi
19		120	12.3	211735	9	AC091564	AC091564 Homo sapi
20		88	9.0	507	6	AX210285	AX210285 Sequence
21		88	9.0	528	6	AX210280	AX210280 Sequence
22	c	88	9.0	111126	9	AF321237	AF321237 Homo sapi
23		64	6.6	650	9	AF399618	AF399618 Homo sapi
24		50	5.1	948	10	AY073646	AY073646 Mus muscu
25		50	5.1	948	10	AY317815	AY317815 Mus muscu
26		50	5.1	194290	10	AC116327	AC116327 Mus muscu
27		50	5.1	239821	2	AC098982	AC098982 Rattus no
28		50	5.1	252192	2	AC147554	AC147554 Mus muscu
29		50	5.1	257621	2	AC094703	AC094703 Rattus no
30		47	4.8	951	10	AY073740	AY073740 Mus muscu
31		47	4.8	951	10	AY317827	AY317827 Mus muscu
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33		47	4.8	269821	2	AC137524	AC137524 Mus muscu
34		41	4.2	943	10	AY074218	AY074218 Mus muscu
35		41	4.2	948	10	AY317825	AY317825 Mus muscu
36		41	4.2	951	10	AY073056	AY073056 Mus muscu
37		41	4.2	951	10	AY317826	AY317826 Mus muscu
38		41	4.2	954	10	AY073498	AY073498 Mus muscu
39		41	4.2	954	10	AY317818	AY317818 Mus muscu
40	c	41	4.2	155781	2	AF321234	AF321234 Mus muscu
41	c	41	4.2	269821	2	AC137524	AC137524 Mus muscu
42	c	40	4.1	239821	2	AC098982	AC098982 Rattus no
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44		38	3.9	960	10	AY317824	AY317824 Mus muscu
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ALIGNMENTS

RESULT 1
AX686711
LOCUS AX686711 977 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 1 from Patent WO02070707.
ACCESSION AX686711
VERSION AX686711.1 GI:29372291
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Padigaru,M., Gerlach,V.L., Smithson,G., Stone,D., Bin-Yang,R.,
Conley,P., Hart,M., Tomlinson,J.E., Topper,J.N., Kekuda,R.,
Casman,S.J., Edinger,S. and Macdougall,J.R.

```
  TITLE     Gpcr-like proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 02070707-A 1 12-SEP-2002;
            Curagen Corporation (US) ; COR THERAPEUTICS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .977
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 977;  DB 6;  Length 977;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  977;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAACTAAAAAAACACATCATGGAGCTCCGGAACTCCACCTTGGGAAGCGGCTTCATCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCAACTAAAAAAACACATCATGGAGCTCCGGAACTCCACCTTGGGAAGCGGCTTCATCTT 60

Qy         61 GGTGGGGATTCTGAATGACAGTGGGTCTCCTGAACTGCTCTATGCTACATTTACAATCCT 120
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Db         61 GGTGGGGATTCTGAATGACAGTGGGTCTCCTGAACTGCTCTATGCTACATTTACAATCCT 120

Qy        121 ATACATGTTGGCACTGACCAGCAATGGTCTGCTGCTCCTGGCCATCACCATAGAAGCCCG 180
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Db        181 GCTCCACATGCCCATGTACCTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCAC 240

Qy        241 ATCTGTTGTCACTCCCAAGGCCTTGGCGGACTTTCTGCGCAGAGAAAACACTATCTCCTT 300
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Db        241 ATCTGTTGTCACTCCCAAGGCCTTGGCGGACTTTCTGCGCAGAGAAAACACTATCTCCTT 300

Qy        301 TGGAGGCTGTGCACTTCAGATGTTCCTGGCACTGACAATGGGTAGCGCTGAGGACCTCCT 360
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Db        301 TGGAGGCTGTGCACTTCAGATGTTCCTGGCACTGACAATGGGTAGCGCTGAGGACCTCCT 360

Qy        361 ACTGGCCTTCATGGCCTATGACAGGTATGTGGCCATTTGTCATCCTCTGAAATACATGAC 420
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Db        361 ACTGGCCTTCATGGCCTATGACAGGTATGTGGCCATTTGTCATCCTCTGAAATACATGAC 420

Qy        421 CCTCATGAGCCCAAGAGTCTGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCT 480
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Qy        481 GATTGCTATAGGACATACCATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAAT 540
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Db        481 GATTGCTATAGGACATACCATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAAT 540

Qy        541 CAGGCATCTGCTCTGTGAGATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAG 600
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Db        541 CAGGCATCTGCTCTGTGAGATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAG 600

Qy        601 GTATGAGCTTATAATATACGTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCAT 660
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Db        601 GTATGAGCTTATAATATACGTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCAT 660

Qy        661 TGTGGCCTCCTACACACTAGTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAG 720
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Db        661 TGTGGCCTCCTACACACTAGTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAG 720

Qy        721 GAAGAAAGCCCTTGTCACCTGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGC 780
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Db        721 GAAGAAAGCCCTTGTCACCTGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGC 780

Qy        781 TGCCACATTCATGTATGTCTTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCAT 840
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Qy        901 TAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTC 960
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Db        901 TAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTC 960

Qy        961 CACGCTCTAGGGAAGGA 977
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Db        961 CACGCTCTAGGGAAGGA 977


RESULT 2
AC091564/c
LOCUS       AC091564               211735 bp    DNA     linear   PRI 03-SEP-2002
DEFINITION  Homo sapiens chromosome 11, clone RP11-732A19, complete sequence.
ACCESSION   AC091564
VERSION     AC091564.12  GI:22657585
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 211735)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 11, clone RP11-732A19
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 211735)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
            Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
            Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K.,
            Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
            Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
            MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
            McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
            Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
            Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
            Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
            Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
            Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
            Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 211735)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
            Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
            Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
            Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
            Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
            Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-AUG-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 211735)
```

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AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
          Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
          Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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          Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
          McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
          Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
          O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
          Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
          Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
          Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
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          Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
          Zembek,L., Zimmer,A. and Zody,M.
TITLE     Direct Submission
JOURNAL   Submitted (03-SEP-2002) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT   On Sep 3, 2002 this sequence version replaced gi:22123080.
          All repeats were identified using RepeatMasker:
          Smit, A.F.A. & Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html
          -------------- Genome Center
              Center: Whitehead Institute/ MIT Center for Genome Research
              Center code: WIBR
              Web site: http://www-seq.wi.mit.edu
              Contact: sequence_submissions@genome.wi.mit.edu
          -------------- Project Information
              Center project name: L11860
              Center clone name: 732_A_19
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                     /rpt_family="AluSg"
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     repeat_region   8518. .8617
                     /rpt_family="MIR"
     repeat_region   9609. .9671
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RESULT 3
AB065539
LOCUS       AB065539               1350 bp    DNA     linear   PRI 23-JUL-2002
DEFINITION  Homo sapiens gene for seven transmembrane helix receptor,
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ACCESSION   AB065539
VERSION     AB065539.1  GI:21928374
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S.,
            Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y.
  TITLE     Genome-wide discovery and analysis of human seven transmembrane
            helix receptor genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1350)
  AUTHORS   Suwa,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research
            Center (CBRC), National Institute of Advanced Industrial Science
            and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
            (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
            Tel:81-3-3599-8080, Fax:81-3-3599-8081)
COMMENT     This sequence is a seven transmembrane helix receptor candidate
            predicted from the whole human genome sequences using our automated
            system that contains programs of gene
            finding(GeneDecoder), sequence search, motif-domain assignment and
            transmembrane helix prediction.
            And the sequence is submitted by the collaborative project between
            [Computational Biology Research Center (CBRC), National Institute
            of Advanced Industrial Science and Technology (AIST)] and [Genome
            Science Division, Research Center for Advanced Science and
            Technology (RCAST), University of Tokyo].
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RESULT 4
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DEFINITION Homo sapiens chromosome 11 clone RP11-732A19, WORKING DRAFT SEQUENCE, 18 unordered pieces.
ACCESSION AC027641
VERSION AC027641.2 GI:8570385
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 208430)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 208430)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT On Jun 17, 2000 this sequence version replaced gi:7344780.

---------- Genome Center ----------
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
---------- Project Information ----------
Center project name: H_NH0732A19
---------- Summary Statistics ----------
Sequencing vector: M13; 98%
Sequencing vector: plasmid; 2%
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 2% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198825 bases at least Q40
Consensus quality: 202103 bases at least Q30
Consensus quality: 203934 bases at least Q20
Insert size: 219000; agarose-fp
Insert size: 206730; sum-of-contigs
Quality coverage: 4.27 in Q20 bases; agarose-fp
Quality coverage: 4.55 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

*	1	1760: contig of 1760 bp in length
*	1761	1860: gap of unknown length
*	1861	3171: contig of 1311 bp in length
*	3172	3271: gap of unknown length
*	3272	5628: contig of 2357 bp in length
*	5629	5728: gap of unknown length
*	5729	7760: contig of 2032 bp in length
*	7761	7860: gap of unknown length
*	7861	15503: contig of 7643 bp in length
*	15504	15603: gap of unknown length
*	15604	18871: contig of 3268 bp in length
*	18872	18971: gap of unknown length
*	18972	22430: contig of 3459 bp in length
*	22431	22530: gap of unknown length
*	22531	28556: contig of 6026 bp in length
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*	35415	35514: gap of unknown length
*	35515	42738: contig of 7224 bp in length
*	42739	42838: gap of unknown length
*	42839	50307: contig of 7469 bp in length
*	50308	50407: gap of unknown length
*	50408	62974: contig of 12567 bp in length
*	62975	63074: gap of unknown length
*	63075	73753: contig of 10679 bp in length
*	73754	73853: gap of unknown length
*	73854	87630: contig of 13777 bp in length
*	87631	87730: gap of unknown length
*	87731	106802: contig of 19072 bp in length
*	106803	106902: gap of unknown length
*	106903	120650: contig of 13748 bp in length
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Qy        541 CAGGCATCTGCTCTGTGAGATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52090 CAGGCATCTGCTCTGTGAGATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAG 52031

Qy        601 GTATGAGCTTATAATATACGTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52030 GTATGAGCTTATAATATACGTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCAT 51971

Qy        661 TGTGGCCTCCTACACACTAGTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51970 TGTGGCCTCCTACACACTAGTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAG 51911

Qy        721 GAAGAAAGCCCTTGTCACCTGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51910 GAAGAAAGCCCTTGTCACCTGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGC 51851

Qy        781 TGCCACATTCATGTATGTCTTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51850 TGCCACATTCATGTATGTCTTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCAT 51791

Qy        841 CTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51790 CTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAA 51731

Qy        901 TAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      51730 TAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTC 51671

Qy        961 CACGCTCTAGGGAAGGA 977
              |||||||||||||||||
Db      51670 CACGCTCTAGGGAAGGA 51654


RESULT 5
AX241682
LOCUS       AX241682                947 bp    DNA     linear   PAT 26-SEP-2001
DEFINITION  Sequence 430 from Patent WO0127158.
ACCESSION   AX241682
VERSION     AX241682.1  GI:15798557
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bellenson,J., Smith,D., Lancet,D., Glusman,G., Fuchs,T. and
            Yanai,I.
  TITLE     Olfactory receptor sequences
  JOURNAL   Patent: WO 0127158-A 430 19-APR-2001;
            Digiscents (US) ; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
FEATURES             Location/Qualifiers
     source          1. .947
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="(H38g279 nucleotide)"
ORIGIN

  Query Match             84.6%;  Score 827;  DB 6;  Length 947;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  947;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         20 ATGGAGCTCCGGAACTCCACCTTGGGAAGCGGCTTCATCTTGGTGGGGATTCTGAATGAC 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCTCCGGAACTCCACCTTGGGAAGCGGCTTCATCTTGGTGGGGATTCTGAATGAC 60

Qy         80 AGTGGGTCTCCTGAACTGCTCTATGCTACATTTACAATCCTATACATGTTGGCACTGACC 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTGGGTCTCCTGAACTGCTCTATGCTACATTTACAATCCTATACATGTTGGCACTGACC 120

Qy        140 AGCAATGGTCTGCTGCTCCTGGCCATCACCATAGAAGCCCGGCTCCACATGCCCATGTAC 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCAATGGTCTGCTGCTCCTGGCCATCACCATAGAAGCCCGGCTCCACATGCCCATGTAC 180

Qy        200 CTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCACATCTGTTGTCACTCCCAAG 259
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Db        181 CTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCACATCTGTTGTCACTCCCAAG 240
Qy        260 GCCTTGGCGGACTTTCTGCGCAGAGAAAACACTATCTCCTTTGGAGGCTGTGCACTTCAG 319
Db        241 GCCTT-GCGGACTTTCTGCGCAGAGAAAACACTATCTCCTTTGGAGGCTGTGCACTTCAG 299
Qy        320 ATGTTCCTGGCACTGACAATGGGTAGCGCTGAGGACCTCCTACTGGCCTTCATGGCCTAT 379
Db        300 ATGTTCCTGGCACTGACAATGGGTAGCGCTGAGGACCTCCTACTGGCCTTCATGGCCTAT 359
Qy        380 GACAGGTATGTGGCCATTTGTCATCCTCTGAAATACATGACCCTCATGAGCCCAAGAGTC 439
Db        360 GACAGGTATGTGGCCATTTGTCATCCTCTGAAATACATGACCCTCATGAGCCCAAGAGTC 419
Qy        440 TGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTGCTATAGGACATACC 499
Db        420 TGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTGCTATAGGACATACC 479
Qy        500 ATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAATCAGGCATCTGCTCTGTGAG 559
Db        480 ATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAATCAGGCATCTGCTCTGTGAG 539
Qy        560 ATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATGAGCTTATAATATAC 619
Db        540 ATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATGAGCTTATAATATAC 599
Qy        620 GTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACACTA 679
Db        600 GTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACACTA 659
Qy        680 GTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCACC 739
Db        660 GTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCACC 719
Qy        740 TGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGCTGCCACATTCATGTATGTC 799
Db        720 TGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGCTGCCACATTCATGTATGTC 779
Qy        800 TTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCATCTCTGTTTTCTACACAATT 859
Db        780 TTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCATCTCTGTTTTCTACACAATT 839
Qy        860 GTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGGGCC 919
Db        840 GTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGGGCC 899
Qy        920 TTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTCCACGCTC 967
Db        900 TTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTCCACGCTC 947
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RESULT 6
AF399487
LOCUS       AF399487                649 bp    DNA     linear   PRI 23-AUG-2001
DEFINITION  Homo sapiens clone OR2AG2P olfactory receptor pseudogene, partial
            sequence.
ACCESSION   AF399487
VERSION     AF399487.1  GI:15282001
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Fuchs,T., Malecova,B., Linhart,C., Sharan,R., Khen,M., Herwig,R.,
            Shmulevich,D., Elkon,R., Steinfath,M., O'Brien,J.K., Radelof,U.,
            Lehrach,H., Olender,Z., Glusman,G., Lancet,D. and Shamir,R.
  TITLE     DEFOG: A Practical Scheme for Deciphering Families of Genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 649)
  AUTHORS   Fuchs,T., Malecova,B., Linhart,C., Sharan,R., Khen,M., Herwig,R.,
            Shmulevich,D., Elkon,R., Steinfath,M., O'Brien,J.K., Radelof,U.,
            Lehrach,H., Olender,Z., Glusman,G., Lancet,D. and Shamir,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Dept. of Molecular Genetics and the Crown
            Human Genome Center, Weizmann Institute of Science, Rehovot 76100,
            Israel
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="OR2AG2P"
     gene            <1. .>649
                     /gene="olfactory receptor"
                     /note="contains transmembrane regions 2-7"
                     /pseudo
ORIGIN
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  Query Match           61.9%;  Score 605;  DB 9;  Length 649;
  Best Local Similarity 100.0%;  Pred. No. 0;
  Matches  605;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        266 GCGGACTTTCTGCGCAGAGAAAACACTATCTCCTTTGGAGGCTGTGCACTTCAGATGTTC 325
Db         45 GCGGACTTTCTGCGCAGAGAAAACACTATCTCCTTTGGAGGCTGTGCACTTCAGATGTTC 104
Qy        326 CTGGCACTGACAATGGGTAGCGCTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGG 385
Db        105 CTGGCACTGACAATGGGTAGCGCTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGG 164
Qy        386 TATGTGGCCATTTGTCATCCTCTGAAATACATGACCCTCATGAGCCCAAGAGTCTGCTGG 445
Db        165 TATGTGGCCATTTGTCATCCTCTGAAATACATGACCCTCATGAGCCCAAGAGTCTGCTGG 224
Qy        446 ATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTGCTATAGGACATACCATGTAC 505
Db        225 ATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTGCTATAGGACATACCATGTAC 284
Qy        506 ACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAATCAGGCATCTGCTCTGTGAGATCCCA 565
Db        285 ACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAATCAGGCATCTGCTCTGTGAGATCCCA 344
Qy        566 CCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATGAGCTTATAATATACGTGACA 625
Db        345 CCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATGAGCTTATAATATACGTGACA 404
Qy        626 GGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACACTAGTCCTA 685
Db        405 GGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACACTAGTCCTA 464
Qy        686 TTCACTGTGCTTCGTATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCACCTGCTCT 745
Db        465 TTCACTGTGCTTCGTATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCACCTGCTCT 524
Qy        746 TCCCACCTGATTGTGGTCGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGCCC 805
Db        525 TCCCACCTGATTGTGGTCGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGCCC 584
Qy        806 AGTTCCTTCCACAGCCCCAAACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACT 865
Db        585 AGTTCCTTCCACAGCCCCAAACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACT 644
Qy        866 CCAGC 870
Db        645 CCAGC 649
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RESULT 7
AX241679
LOCUS       AX241679                948 bp    DNA     linear   PAT 26-SEP-2001
DEFINITION  Sequence 427 from Patent WO0127158.
ACCESSION   AX241679
VERSION     AX241679.1  GI:15798554
KEYWORDS    .
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bellenson,J., Smith,D., Lancet,D., Glusman,G., Fuchs,T. and
            Yanai,I.
  TITLE     Olfactory receptor sequences
  JOURNAL   Patent: WO 0127158-A 427 19-APR-2001;
            Digiscents (US) ; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
FEATURES             Location/Qualifiers
     source          1. .948
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="(H38g276 nucleotide)"
ORIGIN

  Query Match             12.3%;  Score 120;  DB 6;  Length 948;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-58;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926


RESULT 8
AX244613
LOCUS       AX244613                951 bp    DNA     linear   PAT 28-SEP-2001
DEFINITION  Sequence 39 from Patent WO0166742.
ACCESSION   AX244613
VERSION     AX244613.1  GI:15859514
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lal,P., Tang,Y.T., Patterson,C., Yao,M.G., Shih,L.L.,
            Tribouley,C.M., Lu,D.A., Yue,H., Khan,F.A., Policky,J.L.,
            Au-Young,J., Yang,J., Harland,L., Walsh,R.T., Lo,T.P. and
            Borowsky,M.L.
  TITLE     G-protein coupled receptors
  JOURNAL   Patent: WO 0166742-A 39 13-SEP-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .951
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 7472446CB1"
ORIGIN

  Query Match             12.3%;  Score 120;  DB 6;  Length 951;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-58;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926


RESULT 9
AX448455
LOCUS       AX448455                951 bp    DNA     linear   PAT 03-JUL-2002
DEFINITION  Sequence 121 from Patent WO0224726.
ACCESSION   AX448455
VERSION     AX448455.1  GI:21697353
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Veithen,A.
  TITLE     Olfactory and pheromones g-protein coupled receptors
  JOURNAL   Patent: WO 0224726-A 121 28-MAR-2002;
            ChemCom S.A. (BE)
FEATURES             Location/Qualifiers
     source          1. .951
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             1. .951
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD37547.1"
                     /db_xref="GI:21697354"
                     /db_xref="REMTREMBL:CAD37547"
                     /translation="MELWNFTLGSGFILVGILNDSGSPELLCATITILYLLALISNGL
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                     VYTMHYPFCRAQEIRHLLCEIPHLLKVACADTSRYELMVYVMGVTFLIPSLAAILASY
                     TQILLTVLHMPSNEGRKKALVTCSSHLTVVGMFYGAATFMYVLPSSFHSTRQDNIISV
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ORIGIN

  Query Match             12.3%;  Score 120;  DB 6;  Length 951;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-58;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926


RESULT 10
BD144532
LOCUS       BD144532                951 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel G-protein coupled receptors.
ACCESSION   BD144532
VERSION     BD144532.1  GI:27850290
KEYWORDS    JP 2002112793-A/257.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   Haga,T., Takeda,S. and Miyake,N.
  TITLE     Novel G-protein coupled receptors
  JOURNAL   Patent: JP 2002112793-A 257 16-APR-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002112793-A/257
            PD   16-APR-2002
            PF   09-FEB-2001 JP 2001034434
            PI   TATSUYA HAGA,SHIGEKI TAKEDA,NARIKI MIYAKE
            PC
            C12N15/09,A01K67/027,A61K38/00,A61K39/395,A61K39/395,A61K45/00, PC
             A61K48/00,
            PC   A61P43/00,C07K14/705,C07K16/28,C07K19/00,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
            G01N33/566//
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            PC   C12P21/08,C12N15/00,A61K37/02,C12N5/00
            CC   Novel G-protein coupled receptors
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(951).
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           12.3%;  Score 120;  DB 6;  Length 951;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-58;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926


RESULT 11
AX210250
LOCUS       AX210250                1008 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 10 from Patent WO0157215.
ACCESSION   AX210250
VERSION     AX210250.1  GI:15424571
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Padigaru,M., Spytek,K.A., Li,L., Ballinger,R.A., Mishra,V.S. and
            Baumgartner,J.C.
  TITLE     Novel polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0157215-A 10 09-AUG-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           12.3%;  Score 120;  DB 6;  Length 1008;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-58;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 916

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976


RESULT 12
AX551018
LOCUS       AX551018                1008 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 11 from Patent WO0236632.
ACCESSION   AX551018
VERSION     AX551018.1  GI:25814023
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Alsobrook,J.P., Burgess,C.E., Grosse,W.M., Lepley,D.M., Padigaru,M.
            and Spytek,K.A.
  TITLE     Novel single nucleotide polymorphisms for olfactory receptor-like
            polypeptides and nucleic acids encoding the same
  JOURNAL   Patent: WO 0236632-A 11 10-MAY-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1008
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             27. .1001
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD57894.1"
                     /db_xref="GI:25814024"
                     /db_xref="REMTREMBL:CAD57894"
                     /translation="MELWNYHSMELWNFTLGSGFILVGILNDSGSPELLCATITILYL
                     LALISNGLLLLAITMEARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISF
                     GGCALQMFLALTMGGAEDLLLAFMAYDRYVAICHPLTYMTLMSSRACWLMVATSWILA
                     SLSALIYTVYTMHYPFCRAQEIRHLLCEIPHLLKLACADTSRYELMVYVMGVTFLIPS
                     LAAILASYTQILLTVLHMPSNEGRKKALVTCSSHLTVVGMFYGAATFMYVLPSSFHST
                     RQDNIISVFYTIVTPALNPLIYSLRNKEVMRALRRVLGKYMLPAHSTL"
ORIGIN

  Query Match           12.3%;  Score 120;  DB 6;  Length 1008;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-58;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Db        917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976


RESULT 13
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LOCUS       AX551020                1008 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 13 from Patent WO0236632.
ACCESSION   AX551020
VERSION     AX551020.1  GI:25814025
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Alsobrook,J.P., Burgess,C.E., Grosse,W.M., Lepley,D.M., Padigaru,M.
            and Spytek,K.A.
  TITLE     Novel single nucleotide polymorphisms for olfactory receptor-like
            polypeptides and nucleic acids encoding the same
  JOURNAL   Patent: WO 0236632-A 13 10-MAY-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1008
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             27. .1001
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD57895.1"
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                     /db_xref="REMTREMBL:CAD57895"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.8e-58;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976


RESULT 14
AX210248
LOCUS       AX210248               1050 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 8 from Patent WO0157215.
ACCESSION   AX210248
VERSION     AX210248.1  GI:15424570
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Padigaru,M., Spytek,K.A., Li,L., Ballinger,R.A., Mishra,V.S. and
            Baumgartner,J.C.
  TITLE     Novel polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0157215-A 8 09-AUG-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.8e-58;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Db        878 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 937

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 15
AX646083
LOCUS       AX646083               1351 bp    DNA     linear   PAT 04-MAR-2003
DEFINITION  Sequence 275 from Patent EP1270724.
ACCESSION   AX646083
VERSION     AX646083.1  GI:28798462
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Suwa,M., Asai,K., Akiyama,Y. and Aburatani,H.
  TITLE     Guanosine triphosphate-binding protein coupled receptors
  JOURNAL   Patent: EP 1270724-A 275 02-JAN-2003;
            National Institute of Advanced Industrial Science and Technology
            (JP) ; Center for Advanced Science and Technology Incubation, Ltd.
            (JP)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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                     /codon_start=1
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                     /db_xref="GI:28798463"
                     /db_xref="REMTREMBL:CAD69177"
                     /translation="MELWNFTLGSGFILVGILNDSGSPELLCATITILYLLALISNGL
                     LLLAITMEARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMF
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                     VYTMHYPFCRAQEIRHLLCEIPHLLKVACADTSRYELMVYVMGVTFLIPSLAAILASY
                     TQILLTVLHMPSNEGRKKALVTCSSHLTVVGMFYGAATFMYVLPSSFHSTRQDNIISV
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ORIGIN

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Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
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Db       1067 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 1126


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Job time : 3868 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 01:51:45 ; Search time 433 Seconds (without alignments) 9585.426 Million cell updates/sec

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Perfect score: 977
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 20

Total number of hits satisfying chosen parameters: 198

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	977	100.0	977	6	ABQ81238	Abq81238 Human olf
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5	120	12.3	951	5	AAS42307	Aas42307 Human cDN
6	120	12.3	951	6	ABZ43126	Abz43126 Human GPC
7	120	12.3	951	6	ABK68461	Abk68461 Human DNA
8	120	12.3	951	6	ABK37593	Abk37593 DNA encod
9	120	12.3	1008	5	AAS11688	Aas11688 Human odo
10	120	12.3	1008	6	ABK53096	Abk53096 cDNA sequ
11	120	12.3	1008	6	ABK53097	Abk53097 cDNA sequ
12	120	12.3	1050	5	AAS11687	Aas11687 Human odo
13	120	12.3	1351	9	ADC85822	Adc85822 Human GPC
14	27	2.8	678	3	AAA51192	Aaa51192 Murine ol
15	27	2.8	678	7	ACA04914	Aca04914 Mouse odo
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17	26	2.7	26	6	ABT04308	Abt04308 Human G-p
18	26	2.7	932	6	AAD28711	Aad28711 Human G-p
19	26	2.7	964	4	AAH32491	Aah32491 Human olf
20	26	2.7	1337	9	ADC86264	Adc86264 Human GPC
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22	25	2.6	950	9	ADD12838	Add12838 cDNA enco
23	25	2.6	989	4	AAH32334	Aah32334 Human olf
24	25	2.6	1132	7	AAD51230	Aad51230 Human REM
25	25	2.6	1250	9	ADC86390	Adc86390 Human GPC
26	23	2.4	931	9	ADC86616	Adc86616 Human GPC
27	23	2.4	939	4	AAH31803	Aah31803 Human olf
28	23	2.4	945	6	AAF88449	Aaf88449 Human GPC
29	23	2.4	945	9	ADD12820	Add12820 cDNA enco
30	23	2.4	951	5	AAS42275	Aas42275 Human cDN
31	23	2.4	951	6	ABZ43011	Abz43011 Human GPC
32	23	2.4	951	6	ABK68432	Abk68432 Human DNA
33	23	2.4	951	6	ABK37561	Abk37561 DNA encod
34	23	2.4	960	9	ADD12748	Add12748 cDNA enco
35	23	2.4	962	6	AAF88459	Aaf88459 Human GPC
36	23	2.4	962	9	ADD12840	Add12840 cDNA enco
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38	23	2.4	971	6	AAD40634	Aad40634 Human G-p
39	23	2.4	980	6	ABQ88378	Abq88378 Human G p
40	23	2.4	980	6	ABQ88379	Abq88379 Human G p
41	23	2.4	994	4	AAH31675	Aah31675 Human olf
42	23	2.4	1010	9	ADC79399	Adc79399 Human G p
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44	23	2.4	1351	9	ADC85738	Adc85738 Human GPC
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ALIGNMENTS

RESULT 1
ABQ81238
ID ABQ81238 standard; cDNA; 977 BP.
XX
AC ABQ81238;
XX
DT 05-DEC-2002 (first entry)
XX
DE Human olfactory receptor-like protein GPCR1 coding sequence.
XX
KW GPCR1; olfactory receptor; G-protein coupled receptor; receptor; human;
KW antiarteriosclerotic; antidiabetic; analgesic; cytostatic;
KW antidepressant; nootropic; neuroprotective; immunosuppressive;
KW antiallergic; antibacterial; virucide; protozoacide; fungicide;
KW cardiomyopathy; atherosclerosis; diabetes; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 20. .970
FT /*tag= a
FT /product= "GPCR1"
XX
PN WO200270707-A2.
XX
PD 12-SEP-2002.
XX
PF 18-DEC-2001; 2001WO-US049168.
XX
PR 18-DEC-2000; 2000US-0256635P.
XX
PA (CURA-) CURAGEN CORP.
PA (CORT-) COR THERAPEUTICS INC.
XX
PI Padigaru M, Gerlach VL, Smithson G, Stone D, Bin-Yang R;
PI Conley P, Hart M, Tomlinson JE, Topper JN, Kekuda R, Casman SJ;
PI Edinger S, Macdougall JR;
XX
DR WPI; 2002-698753/75.
DR P-PSDB; ABB79908.
XX
PT New G-protein coupled receptor (GPCR1) proteins and nucleic acids, useful
PT for treating or preventing a GPCR1-associated disorder, e.g.
PT cardiomyopathy, atherosclerosis, diabetes, or disorders related to cell
PT signal processing.
XX

PS Claim 8; Page 10; 111pp; English.
XX
CC The present sequence is that of a nucleic acid encoding a novel human G-
CC protein coupled receptor, designated GPCR1, that has structural and
CC physiological functions characteristic of the olfactory receptor family.
CC The invention provides GPCR1 polypeptides, nucleic acids and antibodies.
CC These are useful for treating or preventing a GPCR1-associated disorder,
CC such as cardiomyopathy, atherosclerosis, diabetes, or a disorder related
CC to cell signal processing or metabolic pathway modulation in humans
CC (claimed). They may further be used for treating or preventing e.g.
CC developmental diseases, metabolic pathway disorders, retinal disorders,
CC wasting disorders associated with chronic diseases, pain, cancer,
CC psychotic and neurological disorders (e.g. anxiety or schizophrenia),
CC autoimmune diseases, allergies, bacterial, fungal, protozoal and viral
CC infections, neurodegenerative diseases (e.g. Alzheimer's disease), and
CC haematopoietic diseases. The proteins and nucleic acids may also be used
CC as research tools, as diagnostic or prognostic markers, in gene therapy,
CC for promoting tissue regeneration in vitro and in vivo, and as biological
CC defence weapons. The nucleic acids may also be used in chromosome
CC mapping, in tissue typing, in forensic biology (e.g. to identify
CC individuals from minute biological samples), in forensic identification
CC of a biological sample, as surrogate markers, and in pharmacogenomics
XX
SQ Sequence 977 BP; 215 A; 279 C; 220 G; 263 T; 0 U; 0 Other;

Query Match 100.0%; Score 977; DB 6; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GGTGGGGATTCTGAATGACAGTGGGTCTCCTGAACTGCTCTATGCTACATTTACAATCCT 120
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Db        121 ATACATGTTGGCACTGACCAGCAATGGTCTGCTGCTCCTGGCCATCACCATAGAAGCCCG 180

Qy        181 GCTCCACATGCCCATGTACCTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTCCACATGCCCATGTACCTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCAC 240

Qy        241 ATCTGTTGTCACTCCCAAGGCCTTGGCGGACTTTCTGCGCAGAGAAAACACTATCTCCTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCTGTTGTCACTCCCAAGGCCTTGGCGGACTTTCTGCGCAGAGAAAACACTATCTCCTT 300

Qy        301 TGGAGGCTGTGCACTTCAGATGTTCCTGGCACTGACAATGGGTAGCGCTGAGGACCTCCT 360
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Qy        361 ACTGGCCTTCATGGCCTATGACAGGTATGTGGCCATTTGTCATCCTCTGAAATACATGAC 420
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Qy        481 GATTGCTATAGGACATACCATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAAT 540
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Qy        601 GTATGAGCTTATAATATACGTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        661 TGTGGCCTCCTACACACTAGTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        721 GAAGAAAGCCCTTGTCACCTGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGC 780
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Qy        781 TGCCACATTCATGTATGTCTTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        841 CTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAA 900
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Db        841 CTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAA 900

Qy        901 TAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTC 960
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Qy        961 CACGCTCTAGGGAAGGA 977
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RESULT 2
AAH31857
ID AAH31857 standard; DNA; 947 BP.
XX
AC AAH31857;
XX
DT 30-JUL-2001 (first entry)
XX
DE Human olfactory receptor polynucleotide, SEQ ID NO: 430.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation; ds.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027582.
XX
PR 08-OCT-1999; 99US-0158615P.
PR 24-FEB-2000; 2000US-0184809P.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
XX
PS Claim 8; Page 352; 1857pp; English.
XX
CC The present sequence is one of a number of isolated polynucleotides which
CC encode polypeptides involved in olfactory sensation. The polynucleotides
CC can be used in screening for olfactory agonists and antagonists. The
CC methods allow for the determination of primary scents and the
CC identification of the odour receptors used to detect these primary
CC scents. The methods also enable determination of secondary scents and the
CC identification of combinations of odour receptors that are involved in
CC detecting such secondary scents. This enables the construction of a scent
CC representation (also called a scent fingerprint or scent profile), which
CC may be used to re-create and edit scents. Libraries of olfactory
CC receptors are useful for determining the interaction pattern of a

```
CC   composition with the receptors, and can be used for determining
CC   differences in the olfactory faculties of different individuals
XX
SQ   Sequence 947 BP; 200 A; 274 C; 213 G; 260 T; 0 U; 0 Other;

  Query Match            84.6%;  Score 827;  DB 4;  Length 947;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  947;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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Qy         80 AGTGGGTCTCCTGAACTGCTCTATGCTACATTTACAATCCTATACATGTTGGCACTGACC 139
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Qy        140 AGCAATGGTCTGCTGCTCCTGGCCATCACCATAGAAGCCCGGCTCCACATGCCCATGTAC 199
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Db        121 AGCAATGGTCTGCTGCTCCTGGCCATCACCATAGAAGCCCGGCTCCACATGCCCATGTAC 180

Qy        200 CTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCACATCTGTTGTCACTCCCAAG 259
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Db        181 CTCCTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTCACATCTGTTGTCACTCCCAAG 240

Qy        260 GCCTTGGCGGACTTTCTGCGCAGAGAAAACACTATCTCCTTTGGAGGCTGTGCACTTCAG 319
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTT-GCGGACTTTCTGCGCAGAGAAAACACTATCTCCTTTGGAGGCTGTGCACTTCAG 299

Qy        320 ATGTTCCTGGCACTGACAATGGGTAGCGCTGAGGACCTCCTACTGGCCTTCATGGCCTAT 379
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        380 GACAGGTATGTGGCCATTTGTCATCCTCTGAAATACATGACCCTCATGAGCCCAAGAGTC 439
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GACAGGTATGTGGCCATTTGTCATCCTCTGAAATACATGACCCTCATGAGCCCAAGAGTC 419

Qy        440 TGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTGCTATAGGACATACC 499
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TGCTGGATCATGGTGGCCACATCCTGGATCCTGGCATCCCTGATTGCTATAGGACATACC 479

Qy        500 ATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAATCAGGCATCTGCTCTGTGAG 559
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 ATGTACACTATGCACCTCCCTTTCTGTGTGTCCTGGGAAATCAGGCATCTGCTCTGTGAG 539

Qy        560 ATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATGAGCTTATAATATAC 619
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 ATCCCACCCTTGCTGAAGTTGGCCTGTGCTGATACCTCCAGGTATGAGCTTATAATATAC 599

Qy        620 GTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACACTA 679
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 GTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCTCCTACACACTA 659

Qy        680 GTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCACC 739
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 GTCCTATTCACTGTGCTTCGTATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCACC 719

Qy        740 TGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGCTGCCACATTCATGTATGTC 799
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 TGCTCTTCCCACCTGATTGTGGTCGGGATGTTCTATGGAGCTGCCACATTCATGTATGTC 779

Qy        800 TTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCATCTCTGTTTTCTACACAATT 859
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 TTGCCCAGTTCCTTCCACAGCCCCAAACAAGACAACATCATCTCTGTTTTCTACACAATT 839

Qy        860 GTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGGGCC 919
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 GTCACTCCAGCCCTGAATCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGGGCC 899

Qy        920 TTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTCCACGCTC 967
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 TTGAGGAGGGTCCTGGGAAAATACATACTGCTGGCACATTCCACGCTC 947
```

```
RESULT 3
AAH31854
ID   AAH31854 standard; DNA; 948 BP.
XX
AC   AAH31854;
XX
DT   30-JUL-2001  (first entry)
XX
DE   Human olfactory receptor polynucleotide, SEQ ID NO: 427.
XX
KW   Human; olfactory receptor; OR; primary scent determination;
KW   secondary scent determination; polypeptide library; odour receptor;
KW   scent profile; scent fingerprint; scent representation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200127158-A2.
XX
PD   19-APR-2001.
XX
PF   06-OCT-2000; 2000WO-US027582.
XX
PR   08-OCT-1999;   99US-0158615P.
PR   24-FEB-2000; 2000US-0184809P.
XX
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Bellenson J,  Smith D,  Lancet D,  Glusman G,  Fuchs T,  Yanai I;
XX
DR   WPI; 2001-290713/30.
XX
PT   New polynucleotides which encode polypeptides involved in olfactory
PT   sensation for identifying olfactory agonists and antagonists.
XX
PS   Claim 8; Page 350-351; 1857pp; English.
XX
CC   The present sequence is one of a number of isolated polynucleotides which
CC   encode polypeptides involved in olfactory sensation. The polynucleotides
CC   can be used in screening for olfactory agonists and antagonists. The
CC   methods allow for the determination of primary scents and the
CC   identification of the odour receptors used to detect these primary
CC   scents. The methods also enable determination of secondary scents and the
CC   identification of combinations of odour receptors that are involved in
CC   detecting such secondary scents. This enables the construction of a scent
CC   representation (also called a scent fingerprint or scent profile), which
CC   may be used to re-create and edit scents. Libraries of olfactory
CC   receptors are useful for determining the interaction pattern of a
CC   composition with the receptors, and can be used for determining
CC   differences in the olfactory faculties of different individuals
XX
SQ   Sequence 948 BP; 198 A; 275 C; 217 G; 258 T; 0 U; 0 Other;

  Query Match            12.3%;  Score 120;  DB 4;  Length 948;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-49;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926


RESULT 4
AAS15914
ID   AAS15914 standard; cDNA; 951 BP.
XX
AC   AAS15914;
XX
```

DT 25-JAN-2002 (first entry)
XX
DE DNA encoding G-protein coupled receptor (GCREC) #18.
XX
KW G-protein coupled receptor; GCREC; vaccine; gene therapy;
KW cell proliferation disorder; cancer; arteriosclerosis;
KW neurological disorder; epilepsy; stroke; cardiovascular disorder;
KW hypertension; ischaemic heart disease; gastrointestinal disorder;
KW anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
KW diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
KW schizophrenic disorder; neuroskeletal disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .951
FT /*tag= a
FT /product= "GCREC 18"
FT /note= "G-protein coupled receptor 18"
XX
PN WO200166742-A2.
XX
PD 13-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US006814.
XX
PR 03-MAR-2000; 2000US-0186854P.
PR 10-MAR-2000; 2000US-0188384P.
PR 17-MAR-2000; 2000US-0190453P.
PR 20-MAR-2000; 2000US-0190730P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM;
PI Lu DAM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J, Harland L;
PI Walsh RT, Lo TP, Borowsky ML;
XX
DR WPI; 2001-656776/75.
DR P-PSDB; AAU10317.
XX
PT Novel G-protein coupled receptor polypeptides, for treating and
PT preventing autoimmune/inflammatory disorders, neurological disorders,
PT cell proliferative disorders, cardiovascular disorders and viral
PT infections.
XX
PS Claim 5; Page 139-140; 141pp; English.
XX
CC The invention describes a novel isolated polypeptide, selected from a
CC group of 21 G-protein coupled receptor polypeptides (GCREC) and useful in
CC vaccines and gene therapy. The polypeptide (I) is useful for screening
CC for agonist or antagonist of (I), compounds specifically binding to (I),
CC or compounds that modulate the activity of (I). The polynucleotide
CC encoding (1) is useful for screening a compound for effectiveness in
CC altering expression of a target polynucleotide comprising (II), by
CC exposing a sample comprising the target polynucleotide to a compound,
CC detecting altered expression of the target polynucleotide, and comparing
CC the expression of the target polynucleotide in the presence of varying
CC amounts of compound and in the absence of the compound. (I) and (II) are
CC useful for diagnosis, treatment and prevention of cell proliferative
CC disorders (e.g. cancers, arteriosclerosis, atherosclerosis), neurological
CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and
CC neuroskeletal disorders), cardiovascular disorders (e.g. hypertension,
CC ischaemic heart disease), gastrointestinal disorders (e.g. anorexia,
CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,
CC osteoporosis, psoriasis), and metabolic disorders such as obesity.
CC Furthermore, the polynucleotide is useful; as primers for detecting
CC single nucleotide polymorphisms; as elements in microarray, to monitor or
CC measure protein-protein interactions, drug-target interactions, and gene
CC expression profiles; to generate a transcript image of a tissue or cell
CC type, and to generate hybridisation probes useful in mapping the
CC naturally occurring genomic sequence. This sequence encodes G-protein
CC coupled receptor 18, one of 21 GCREC proteins described in the method of
CC the invention
XX
SQ Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

Query Match 12.3%; Score 120; DB 5; Length 951;
Best Local Similarity 100.0%; Pred. No. 3.2e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy 886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926

RESULT 5
AAS42307
ID AAS42307 standard; cDNA; 951 BP.
XX
AC AAS42307;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding olfactory receptor AOLFR107.
XX
KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
KW ss; food additive; cosmetic; fragrance; pharmaceutical additive.
XX
OS Homo sapiens.
XX
PN WO200168805-A2.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US007771.
XX
PR 13-MAR-2000; 2000US-0188914P.
PR 24-MAR-2000; 2000US-0192033P.
PR 12-APR-2000; 2000US-0198474P.
PR 24-APR-2000; 2000US-0199335P.
PR 26-MAY-2000; 2000US-0207702P.
PR 23-JUN-2000; 2000US-0213849P.
PR 16-AUG-2000; 2000US-0226534P.
PR 07-SEP-2000; 2000US-0230732P.
PR 07-FEB-2001; 2001US-0266862P.
XX
PA (SENO-) SENOMYX INC.
XX
PI Zozulya S;
XX
DR WPI; 2001-570867/64.
DR P-PSDB; AAU24614.
XX
PT Nucleic acids encoding human olfactory G protein-coupled receptors,
PT useful for screening for compounds involved in olfactory sensation, where
PT the compounds can be used in the food, pharmaceutical and cosmetic
PT industries to customize odors.
XX
PS Claim 1; Page 128; 319pp; English.
XX
CC The invention relates to nucleic acids encoding human olfactory
CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
CC specifically recognise molecules, odourants, that elicit specific
CC olfactory sensation. The human olfactory receptors and polynucleotides
CC encoding them are useful for screening a library of chemical compounds
CC for compounds that are involved in olfactory sensation. Modulators of
CC their activity are useful for pharmacological and genetic modulation of
CC olfactory signalling pathways. Therefore, they can be used in the food,
CC pharmaceutical and cosmetic industries to customise odours and
CC fragrances. The present sequence encodes a human olfactory receptor of
CC the invention
XX

```
SQ   Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

  Query Match           12.3%;  Score 120;  DB 5;  Length 951;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-49;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926


RESULT 6
ABZ43126
ID   ABZ43126 standard; DNA; 951 BP.
XX
AC   ABZ43126;
XX
DT   06-MAR-2003  (first entry)
XX
DE   Human GPCR polynucleotide SEQ ID NO 513.
XX
KW   Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW   drug development; gustatory; taste; fragrance; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200216548-A2.
XX
PD   28-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-IB001446.
XX
PR   04-AUG-2000; 2000JP-00237818.
PR   13-FEB-2001; 2001JP-00034434.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Haga T,  Takeda S,  Mitaku S;
XX
DR   WPI; 2002-304118/34.
DR   P-PSDB; ABP95852.
XX
PT   Database global search for G protein-coupled receptors, proteins and
PT   encoded genes for studying in vivo signal transduction mechanism and
PT   identifying targets for drug development.
XX
PS   Claim 9; SEQ ID NO 513; 97pp + Sequence Listing; Japanese.
XX
CC   The invention relates to a method for screening G protein-coupled
CC   receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
CC   ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC   domains with 250-1000 amino acid residues to give a gene homologous with
CC   a known GPCR gene. The receptor proteins and encoded genes are useful for
CC   studying in vivo signal transduction mechanism and identifying targets
CC   for drug development e.g. based on olfactory and gustatory receptors in
CC   form of agonists and antagonists by screening intrinsic and extrinsic
CC   ligands as bitter taste inhibitors, taste enhancers and fragrance
CC   improvers. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

  Query Match           12.3%;  Score 120;  DB 6;  Length 951;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-49;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926


RESULT 7
ABK68461
ID   ABK68461 standard; DNA; 951 BP.
XX
AC   ABK68461;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human DNA for olfactory and pheromone G protein-coupled receptor #61.
XX
KW   Human; ds; gene; olfactory and pheromone G protein coupled receptor;
KW   GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
KW   anorectic; taste; fragrance; food additive; cosmetic; cell migration;
KW   sterility; psychotic disorder; neurological disorder; anxiety;
KW   schizophrenia; manic depression; depression; axonal growth;
KW   menstrual cycle; appetite sexual motivation; sexual attraction;
KW   aggression.
XX
OS   Homo sapiens.
XX
PN   WO200224726-A2.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-BE000162.
XX
PR   22-SEP-2000; 2000EP-00870211.
XX
PA   (CHEM-) CHEMCOM SA.
XX
PI   Veithen A;
XX
DR   WPI; 2002-330013/36.
DR   P-PSDB; AAU95574.
XX
PT   Novel pheromone G-protein coupled receptor and receptor-derived agonists,
PT   antagonists or inhibitors useful in food or cosmetic products or in the
PT   treatment or prevention of neurological disorders such as anxiety and
PT   schizophrenia.
XX
PS   Disclosure; Page 196-197; 833pp; English.
XX
CC   The invention relates to olfactory and Pheromone G-protein coupled
CC   receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
CC   portion and its encoding polynucleotide. Also included are an agonist,
CC   antagonist or inhibitor of the GPCR or the polynucleotide, a vector
CC   comprising the polynucleotide, a cell transformed by the vector, a non-
CC   human mammal comprising a partial or total deletion of the polynucleotide
CC   encoding the receptor and screening (detection and possibly, recovering)
CC   of compounds which are known or not known to be agonist, antagonists or
CC   inhibitors of natural compounds to the GPCR. The receptor-derived
CC   agonists, antagonists, inhibitors or compounds are used as an
CC   improvement, elimination or substitution of an existing taste and/or a
CC   fragrance of (or in) the food and/or cosmetic products. They can also be
CC   used in the preparation of medicament in the treatment and/or prevention
CC   of a mammalian disorder, such as cell migration, sterility, psychotic and
CC   neurological disorders, including anxiety, schizophrenia, manic
CC   depression, depression, for promoting axonal growth, nerve cell
CC   connection and nerve regeneration for modulating male and female
CC   endocrine functions, hormone production and the menstrual cycle, for the
CC   prevention or the treatment by stimulation of several mammalian
CC   behaviours, such as stimulation or suppression of appetite, sexual
CC   motivation, sexual attraction, aggression and for promoting or
CC   suppressing chemical communication between organisms. The present
CC   sequence is a human DNA encoding an olfactory and pheromone GPCR
XX
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SQ   Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

  Query Match            12.3%;  Score 120;  DB 6;  Length 951;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-49;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926


RESULT 8
ABK37593
ID   ABK37593 standard; cDNA; 951 BP.
XX
AC   ABK37593;
XX
DT   08-MAY-2002  (first entry)
XX
DE   DNA encoding G-coupled olfactory receptor #95.
XX
KW   Human; olfactory G-coupled receptor; sensory perception of odourant;
KW   odour composition; taste composition; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200198526-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020122.
XX
PR   22-JUN-2000; 2000US-0213812P.
PR   13-MAR-2001; 2001US-00804291.
XX
PA   (SENO-) SENOMYX INC.
XX
PI   Zozulya S,  Stryer L;
XX
DR   WPI; 2002-083330/11.
DR   P-PSDB; AAU85234.
XX
PT   Representing sensory perception of one or more odorants for the
PT   identification and design of tastes and odors comprises providing a
PT   representative group of n olfactory receptors.
XX
PS   Example; Page 101; 182pp; English.
XX
CC   The invention relates to a method of representing sensory perception of
CC   one or more odourants. The method comprises: (a) providing a
CC   representative class of n olfactory receptors or ligand binding domains
CC   (LBD) of these receptors; (b) measuring values X1 to Xn representative of
CC   at least one activity of one or more odourants selected from: (i) binding
CC   one or more odourants to the LBD of at least one of the n olfactory
CC   receptors; (ii) activating at least one of the n olfactory receptors with
CC   the one or more odourants; and (iii) blocking at least one of the n
CC   olfactory receptors with the one or more odourants; and (c) generating a
CC   representation of sensory perception from the values X1 to Xn. The
CC   representation of the sensory perception of odourants is useful for the
CC   design and formulation of odour and taste compositions. ABK37499-ABK37754
CC   and ABK37918-ABK37921 represent human olfactory G-coupled receptor coding
CC   sequences and related PCR primers of the invention
XX
SQ   Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

  Query Match            12.3%;  Score 120;  DB 6;  Length 951;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-49;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 866

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 926


RESULT 9
AAS11688
ID   AAS11688 standard; DNA; 1008 BP.
XX
AC   AAS11688;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human odorant receptor (OR) DNA #5.
XX
KW   Human; olfactory receptor; OR; G-protein coupled receptor superfamily;
KW   GPCR; gene therapy; tranquiliser; vulnerary; anti-HIV; cytostatic; ds;
KW   nootropic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;
KW   antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
KW   human immunodeficiency virus; neoplastic growth; neurological disorder;
KW   Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
KW   wound healing; asthma; Albright hereditary osteodystrophy;
KW   multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             27. .1001
FT                   /*tag=  a
FT                   /product= "Human odorant receptor protein #5"
XX
PN   WO200157215-A2.
XX
PD   09-AUG-2001.
XX
PF   07-FEB-2001; 2001WO-US003923.
XX
PR   07-FEB-2000; 2000US-0180511P.
PR   07-FEB-2000; 2000US-0180630P.
PR   07-FEB-2000; 2000US-0180646P.
PR   08-FEB-2000; 2000US-0180930P.
PR   08-FEB-2000; 2000US-0181004P.
PR   08-FEB-2000; 2000US-0181013P.
PR   08-FEB-2000; 2000US-0181043P.
PR   24-JUL-2000; 2000US-0220262P.
PR   25-JUL-2000; 2000US-0220594P.
PR   11-AUG-2000; 2000US-0224596P.
PR   02-NOV-2000; 2000US-0245292P.
PR   06-FEB-2001; 2001US-00777789.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Padigaru M,  Spytek KA,  Li L,  Ballinger RA,  Mishra VS;
PI   Baumgartner JC;
XX
DR   WPI; 2001-488883/53.
DR   P-PSDB; AAU07088.
XX
PT   Novel isolated NOVX polypeptide related to human odorant receptor family
PT   of G-protein coupled receptor superfamily of proteins useful for treating
PT   trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
XX
PS   Claim 9; Page 44; 199pp; English.
XX
CC   Novel isolated NOVX polynucleotides and their encoded polypeptides of the
CC   invention are related to the human olfactory (or odorant) receptors
CC   (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
CC   sequences are useful for treating or preventing a pathology associated
CC   with OR in a subject, and for manufacturing a medicament for treating a
```

```
CC   syndrome associated with a human disease. These diseases include
CC   disorders of olfactory loss, such as trauma, HIV illness and neoplastic
CC   growth, neurological disorders, such as Parkinson's disease and
CC   Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
CC   disease, multiple sclerosis, and Albright hereditary osteodystrophy. The
CC   polynucleotides and polypeptides are also useful, to identify proteins of
CC   the same family, to screen for molecules which inhibit or enhance the
CC   activity or function of olfactory receptors, to detect nasal epithelial
CC   neuronal tissue, in production of transgenic plants and for the
CC   development of new drug targets for various disorders. This sequence
CC   represents DNA encoding a human OR protein
XX
SQ   Sequence 1008 BP; 216 A; 289 C; 234 G; 269 T; 0 U; 0 Other;

  Query Match           12.3%;  Score 120;  DB 5;  Length 1008;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-49;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 916

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976


RESULT 10
ABK53096
ID   ABK53096 standard; cDNA; 1008 BP.
XX
AC   ABK53096;
XX
DT   15-AUG-2002  (first entry)
XX
DE   cDNA sequence encoding novel odourant receptor NOV6 protein.
XX
KW   NOV; odourant receptor; G protein coupled receptor; GPCR; trauma; HIV;
KW   ss; gene; olfactory receptor; olfactory loss; neoplastic growth;
KW   human immunodeficiency virus; Alzheimer's disease; neurological disorder;
KW   Parkinson's disease.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             27. .1001
FT                   /*tag=  a
FT                   /product= "NOV6 protein"
XX
PN   WO200236632-A2.
XX
PD   10-MAY-2002.
XX
PF   09-OCT-2001; 2001WO-US031744.
XX
PR   02-NOV-2000; 2000US-0245292P.
PR   06-FEB-2001; 2001US-00777789.
PR   20-SEP-2001; 2001US-00245292.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Alsobrook JP,  Burgess CE,  Grosse WM,  Lepley DM,  Padigaru M;
PI   Spytek KA;
XX
DR   WPI; 2002-471499/50.
DR   P-PSDB; AAU97927.
XX
PT   New isolated olfactory receptor-like polypeptide, NOVX, useful for
PT   diagnosing, preventing or treating disorders of olfactory loss, e.g.
PT   trauma, human immunodeficiency virus illness, neoplastic growth and
PT   neurological disorders.
XX
PS   Claim 9; Page 33; 122pp; English.
XX
CC   This invention relates to the DNA and protein sequences of a novel
CC   isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
CC   sequences of the invention and an antibody specific for the protein are
CC   useful for treating or preventing a disorder associated with NOV1 in a
CC   subject, preferably human. A NOVX specific antibody is useful for
CC   determining the presence or amount of protein in a sample. The DNA,
CC   protein and antibody of the invention is useful for diagnosing,
CC   preventing or treating disorders associated with aberrant NOVX expression
CC   such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
CC   virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
CC   Parkinson's disease and Alzheimer's disease. The sequences and NOV
CC   antibody is useful in screening assays, detection assays (e.g.,
CC   chromosomal mapping, tissue typing, forensic biology), predictive
CC   medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
CC   trials and pharmacogenomic), and in methods of treatment (e.g.,
CC   therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC   produce antibodies immunospecific for the protein, to screen for
CC   potential agonist and antagonist compounds, and as bait protein in a two-
CC   hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC   therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
CC   in a NOVX gene, and to modulate NOVX activity. The antibody of the
CC   invention is useful for isolating, and purifying the protein and to
CC   monitor protein levels in tissue as part of a clinical testing procedure.
CC   The present sequence represents the cDNA encoding the NOV6 protein of the
CC   invention
XX
SQ   Sequence 1008 BP; 216 A; 289 C; 234 G; 269 T; 0 U; 0 Other;

  Query Match           12.3%;  Score 120;  DB 6;  Length 1008;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-49;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 916

Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976


RESULT 11
ABK53097
ID   ABK53097 standard; cDNA; 1008 BP.
XX
AC   ABK53097;
XX
DT   15-AUG-2002  (first entry)
XX
DE   cDNA sequence encoding novel odourant receptor NOV7 protein.
XX
KW   NOV; odourant receptor; G protein coupled receptor; GPCR; trauma; HIV;
KW   ss; gene; olfactory receptor; olfactory loss; neoplastic growth;
KW   human immunodeficiency virus; Alzheimer's disease; SNP;
KW   neurological disorder; Parkinson's disease.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             27. .1001
FT                   /*tag=  a
FT                   /product= "NOV7 protein"
FT   variation       replace(278,T)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200236632-A2.
XX
PD   10-MAY-2002.
XX
PF   09-OCT-2001; 2001WO-US031744.
XX
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PR 02-NOV-2000; 2000US-0245292P.
PR 06-FEB-2001; 2001US-00777789.
PR 20-SEP-2001; 2001US-00245292.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Burgess CE, Grosse WM, Lepley DM, Padigaru M;
PI Spytek KA;
XX
DR WPI; 2002-471499/50.
DR P-PSDB; AAU97928.
XX
PT New isolated olfactory receptor-like polypeptide, NOVX, useful for
PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
PT trauma, human immunodeficiency virus illness, neoplastic growth and
PT neurological disorders.
XX
PS Claim 9; Page 34; 122pp; English.
XX
CC This invention relates to the DNA and protein sequences of a novel
CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
CC sequences of the invention and an antibody specific for the protein are
CC useful for treating or preventing a disorder associated with NOV1 in a
CC subject, preferably human. A NOVX specific antibody is useful for
CC determining the presence or amount of protein in a sample. The DNA,
CC protein and antibody of the invention is useful for diagnosing,
CC preventing or treating disorders associated with aberrant NOVX expression
CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
CC antibody is useful in screening assays, detection assays (e.g.,
CC chromosomal mapping, tissue typing, forensic biology), predictive
CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
CC trials and pharmacogenomic), and in methods of treatment (e.g.,
CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC produce antibodies immunospecific for the protein, to screen for
CC potential agonist and antagonist compounds, and as bait protein in a two-
CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
CC invention is useful for isolating, and purifying the protein and to
CC monitor protein levels in tissue as part of a clinical testing procedure.
CC The present sequence represents the cDNA encoding the NOV7 protein of the
CC invention
XX
SQ Sequence 1008 BP; 216 A; 290 C; 234 G; 268 T; 0 U; 0 Other;

Query Match 12.3%; Score 120; DB 6; Length 1008;
Best Local Similarity 100.0%; Pred. No. 3.2e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 857 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 916

Qy 886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 917 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 976

RESULT 12
AAS11687
ID AAS11687 standard; DNA; 1050 BP.
XX
AC AAS11687;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human odorant receptor (OR) DNA #4.
XX
KW Human; olfactory receptor; OR; G-protein coupled receptor superfamily;
KW GPCR; gene therapy; tranquiliser; vulnerary; anti-HIV; cytostatic; ds;
KW nootropic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;
KW antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
KW human immunodeficiency virus; neoplastic growth; neurological disorder;
KW Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
KW wound healing; asthma; Albright hereditary osteodystrophy;
KW multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 72. .1022
FT /*tag= a
FT /product= "Human odorant receptor protein #4"
XX
PN WO200157215-A2.
XX
PD 09-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003923.
XX
PR 07-FEB-2000; 2000US-0180511P.
PR 07-FEB-2000; 2000US-0180630P.
PR 07-FEB-2000; 2000US-0180646P.
PR 08-FEB-2000; 2000US-0180930P.
PR 08-FEB-2000; 2000US-0181004P.
PR 08-FEB-2000; 2000US-0181013P.
PR 08-FEB-2000; 2000US-0181043P.
PR 24-JUL-2000; 2000US-0220262P.
PR 25-JUL-2000; 2000US-0220594P.
PR 11-AUG-2000; 2000US-0224596P.
PR 02-NOV-2000; 2000US-0245292P.
PR 06-FEB-2001; 2001US-00777789.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS;
PI Baumgartner JC;
XX
DR WPI; 2001-488883/53.
DR P-PSDB; AAU07087.
XX
PT Novel isolated NOVX polypeptide related to human odorant receptor family
PT of G-protein coupled receptor superfamily of proteins useful for treating
PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
XX
PS Claim 9; Page 39; 199pp; English.
XX
CC Novel isolated NOVX polynucleotides and their encoded polypeptides of the
CC invention are related to the human olfactory (or odorant) receptors
CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
CC sequences are useful for treating or preventing a pathology associated
CC with OR in a subject, and for manufacturing a medicament for treating a
CC syndrome associated with a human disease. These diseases include
CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
CC growth, neurological disorders, such as Parkinson's disease and
CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
CC disease, multiple sclerosis, and Albright hereditary osteodystrophy. The
CC polynucleotides and polypeptides are also useful, to identify proteins of
CC the same family, to screen for molecules which inhibit or enhance the
CC activity or function of olfactory receptors, to detect nasal epithelial
CC neuronal tissue, in production of transgenic plants and for the
CC development of new drug targets for various disorders. This sequence
CC represents DNA encoding a human OR protein
XX
SQ Sequence 1050 BP; 234 A; 293 C; 238 G; 285 T; 0 U; 0 Other;

Query Match 12.3%; Score 120; DB 5; Length 1050;
Best Local Similarity 100.0%; Pred. No. 3.2e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 878 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 937

```
Qy        886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        938 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 997
```

RESULT 13
ADC85822
ID ADC85822 standard; DNA; 1351 BP.
XX
AC ADC85822;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR gene SEQ ID NO:275.
XX
KW ds; gene; human; GPCR;
KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
DR WPI; 2003-315783/31.
DR P-PSDB; ADC85823.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 1; SEQ ID NO 275; 28pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
CC invention.
XX
SQ Sequence 1351 BP; 342 A; 340 C; 295 G; 374 T; 0 U; 0 Other;

```
  Query Match             12.3%;  Score 120;  DB 9;  Length 1351;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-49;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         826 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 885
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Db        1007 ACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAATCCACTCAT 1066

Qy         886 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 945
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1067 CTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCCTGGGAAAATACAT 1126
```

RESULT 14
AAA51192
ID AAA51192 standard; cDNA; 678 BP.
XX
AC AAA51192;
XX
DT 26-SEP-2000 (first entry)
XX
DE Murine olfactory receptor ligand-binding region cDNA 18.
XX
KW Degenerate primer; ligand-binding region; olfactory receptor;
KW Transmembrane domain; N-terminal; plasma membrane; translocation domain;
KW human rhodopsin receptor; odorant; toxicity; olfactory response; ss.
XX
OS Mus musculus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .669
FT   /*tag= a
FT   /product= "Olfactory_receptor_ligand_binding_protein"
FT   /partial
XX
PN WO200035274-A1.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US030221.
XX
PR 17-DEC-1998; 98US-00112605.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Reed RR, Krautwurst D, Yau KW;
XX
DR WPI; 2000-431471/37.
DR P-PSDB; AAY96679.
XX
PT Primer pair for amplifying olfactory receptor nucleic acid, useful e.g.
PT for producing receptor libraries used in e.g. screening odorants for
PT toxicity.
XX
PS Claim 18; Page 36-37; 61pp; English.
XX
CC AAA51175-93 encode murine odorant/ligand binding regions of olfactory
CC receptors. They were amplified using degenerate primers shown in AAA51163
CC -64. The primers can be used to generate a library of OR-LBR comprising
CC the transmembrane domains (TMD) II-VI, III-VI, II-VII or III-VII.
CC Chimeric nucleic acids encoding a 7-TMD protein comprise a sequence
CC encoding an N-terminal plasma membrane translocation domain (especially
CC the sequence shown in AAY96658), a first TMD and the OR-LBR. The
CC translocation domain was initially derived from the N-terminus of the
CC human rhodopsin receptor. LBR produced by amplification with the primers
CC are useful for generating new odorants, to screen for toxicity or
CC therapeutic activity in odorants, and altering an animal's olfactory
CC response (claimed)
XX
SQ Sequence 678 BP; 148 A; 174 C; 119 G; 237 T; 0 U; 0 Other;

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  Query Match             2.8%;  Score 27;  DB 3;  Length 678;
  Best Local Similarity   100.0%;  Pred. No. 0.0069;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         370 CATGGCCTATGACAGGTATGTGGCCAT 396
               ||||||||||||||||||||||||||
Db         162 CATGGCCTATGACAGGTATGTGGCCAT 188
```

RESULT 15
ACA04914
ID ACA04914 standard; cDNA; 678 BP.
XX
AC ACA04914;
XX
DT 28-MAY-2003 (first entry)
XX
DE Mouse odourant/ligand binding region cDNA #18.
XX
KW ss; olfactory receptor; odourant; ligand-binding region; mouse;
KW olfactory neuron; olfactory epithelium; 7 transmembrane receptor;
KW olfactory response.

XX
OS Mus musculus.
XX
PN US6492143-B1.
XX
PD 10-DEC-2002.
XX
PF 17-DEC-1999; 99US-00465901.
XX
PR 17-DEC-1998; 98US-0112605P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Reed RR, Yau K, Krautwurst D;
XX
DR WPI; 2003-327314/31.
DR P-PSDB; ABU67259.
XX
PT Novel amplification primer sequence pair for amplifying nucleic acid
PT encoding an olfactory receptor ligand-binding region.
XX
PS Example 1; Col 77-80; 46pp; English.
XX
CC The invention relates to an amplification primer sequence pair for
CC amplifying a nucleic acid encoding an olfactory receptor ligand-binding
CC region, comprising a primers appearing as ACA04888 and ACA04889. Also
CC included is a kit for amplifying olfactory receptor sequences comprising
CC the primers. The primers are useful for generating a nucleic acid
CC sequence that encodes a ligand-binding region of an olfactory receptor.
CC The amplified nucleic acid is genomic DNA, mRNA or cDNA derived from
CC olfactory neurons or the olfactory epithelium. The olfactory receptors
CC are 7 transmembrane receptors, manipulation of which can modulate an
CC animals olfactory response and can be used to generate novel odourants.
CC The present sequence encodes a mouse olfactory receptor ligand binding
CC region and is isolated using the primer of the invention
XX
SQ Sequence 678 BP; 148 A; 174 C; 119 G; 237 T; 0 U; 0 Other;

Query Match 2.8%; Score 27; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 CATGGCCTATGACAGGTATGTGGCCAT 396
||||||||||||||||||||||||||
Db 162 CATGGCCTATGACAGGTATGTGGCCAT 188

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Job time : 436 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 6, 2004, 03:31:21 ; Search time 102 Seconds
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Perfect score: 977
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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 20

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	2.8	678	4	US-09-465-901-45	Sequence 45, Appl
2	22	2.3	951	4	US-09-465-901-47	Sequence 47, Appl
c 3	22	2.3	1320	1	US-08-599-252-84	Sequence 84, Appl
c 4	22	2.3	1320	1	US-08-436-074-57	Sequence 57, Appl
c 5	22	2.3	1320	5	PCT-US96-06352-84	Sequence 84, Appl
c 6	22	2.3	1320	5	PCT-US96-06583-84	Sequence 84, Appl
c 7	20	2.0	3383	3	US-08-884-324-12	Sequence 12, Appl
c 8	20	2.0	11464	3	US-08-884-324-13	Sequence 13, Appl
c 9	20	2.0	28994	3	US-08-884-324-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-465-901-45
; Sequence 45, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expession Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-45

Query Match 2.8%; Score 27; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 CATGGCCTATGACAGGTATGTGGCCAT 396
||||||||||||||||||||||||||||
Db 162 CATGGCCTATGACAGGTATGTGGCCAT 188

RESULT 2
US-09-465-901-47
; Sequence 47, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expession Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-47

Query Match 2.3%; Score 22; DB 4; Length 951;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 379 TGACAGGTATGTGGCCATTTGT 400
||||||||||||||||||||||
Db 354 TGACAGGTATGTGGCCATTTGT 375

RESULT 3
US-08-599-252-84/c
; Sequence 84, Application US/08599252
; Patent No. 5705343
; GENERAL INFORMATION:
; APPLICANT: DRAYNA, DENNIS T.
; APPLICANT: FEDER, JOHN N.
; APPLICANT: GNIRKE, ANDREAS
; APPLICANT: KIMMEL, BRUCE E.
; APPLICANT: THOMAS, WINSTON J.
; APPLICANT: WOLFF, ROGER K.
; TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
; TITLE OF INVENTION: HEMOCHROMATOSIS
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington

```
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20006-1888
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/599,252
;       FILING DATE:  09-FEB-1996
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MURASHIGE, KATE H.
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  9053-0001.21
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 887-1500
;       TELEFAX:  (202) 887-0763
;       TELEX:  90-4030
;   INFORMATION FOR SEQ ID NO:  84:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1320 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-599-252-84

  Query Match             2.3%;  Score 22;  DB 1;  Length 1320;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        846 TTTTCTACACAATTGTCACTCC 867
              |||||||||||||||||||||
Db       1210 TTTTCTACACAATTGTCACTCC 1189


RESULT 4
US-08-436-074-57/c
; Sequence 57, Application US/08436074
; Patent No. 5753438
;  GENERAL INFORMATION:
;    APPLICANT:  DRAYNA, DENNIS T.
;    APPLICANT:  FEDER, JOHN N.
;    APPLICANT:  GNIRKE, ANDREAS
;    APPLICANT:  KIMMEL, BRUCE E.
;    APPLICANT:  THOMAS, WINSTON J.
;    APPLICANT:  WOLFF, ROGER K.
;    TITLE OF INVENTION:  METHOD TO DIAGNOSE HEREDITARY
;    TITLE OF INVENTION:  HEMOCHROMATOSIS
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/436,074
;      FILING DATE:  08-MAY-1995
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  9053-0001.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1320 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-436-074-57

  Query Match             2.3%;  Score 22;  DB 1;  Length 1320;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        846 TTTTCTACACAATTGTCACTCC 867
              |||||||||||||||||||||
Db       1210 TTTTCTACACAATTGTCACTCC 1189


RESULT 5
PCT-US96-06352-84/c
; Sequence 84, Application PC/TUS9606352
;  GENERAL INFORMATION:
;    APPLICANT:  DRAYNA, DENNIS T.
;    APPLICANT:  FEDER, JOHN N.
;    APPLICANT:  GNIRKE, ANDREAS
;    APPLICANT:  KIMMEL, BRUCE E.
;    APPLICANT:  THOMAS, WINSTON J.
;    APPLICANT:  WOLFF, ROGER K.
;    TITLE OF INVENTION:  METHOD TO DIAGNOSE HEREDITARY
;    TITLE OF INVENTION:  HEMOCHROMATOSIS
;    NUMBER OF SEQUENCES:  124
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/06352
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/599,252
;      FILING DATE:  09-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  9053-0001.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1320 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US96-06352-84

  Query Match             2.3%;  Score 22;  DB 5;  Length 1320;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        846 TTTTCTACACAATTGTCACTCC 867
              |||||||||||||||||||||
```

```
Db       1210 TTTTCTACACAATTGTCACTCC 1189


RESULT 6
PCT-US96-06583-84/c
; Sequence 84, Application PC/TUS9606583
;  GENERAL INFORMATION:
;    APPLICANT:  DRAYNA, DENNIS T.
;    APPLICANT:  FEDER, JOHN N.
;    APPLICANT:  GNIRKE, ANDREAS
;    APPLICANT:  KIMMEL, BRUCE E.
;    APPLICANT:  THOMAS, WINSTON J.
;    APPLICANT:  WOLFF, ROGER K.
;    TITLE OF INVENTION:  METHOD TO DIAGNOSE HEREDITARY
;    TITLE OF INVENTION:  HEMOCHROMATOSIS
;    NUMBER OF SEQUENCES:  124
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/06583
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/599,252
;      FILING DATE:  09-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  9053-0001.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1320 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US96-06583-84

  Query Match             2.3%;  Score 22;  DB 5;  Length 1320;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        846 TTTTCTACACAATTGTCACTCC 867
              ||||||||||||||||||||||
Db       1210 TTTTCTACACAATTGTCACTCC 1189


RESULT 7
US-08-884-324-12/c
; Sequence 12, Application US/08884324
; Patent No. 6060283
;  GENERAL INFORMATION:
;    APPLICANT:  Takanori OKURA
;    APPLICANT:  Kakuji TORIGOE
;    APPLICANT:  Masahi KURIMOTO
;    TITLE OF INVENTION:  GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
;    TITLE OF INVENTION:  OF INDUCING THE PRODUCTION OF INTERFERON-
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent In Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/884,324
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 185,305/96
;      FILING DATE:  27-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  OKURA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3383 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;      TISSUE TYPE:  placenta
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  1..3383
;      IDENTIFICATION METHOD:  E
US-08-884-324-12

  Query Match             2.0%;  Score 20;  DB 3;  Length 3383;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        831 ACAACATCATCTCTGTTTTC 850
              ||||||||||||||||||||
Db       2761 ACAACATCATCTCTGTTTTC 2742


RESULT 8
US-08-884-324-13/c
; Sequence 13, Application US/08884324
; Patent No. 6060283
;  GENERAL INFORMATION:
;    APPLICANT:  Takanori OKURA
;    APPLICANT:  Kakuji TORIGOE
;    APPLICANT:  Masahi KURIMOTO
;    TITLE OF INVENTION:  GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
;    TITLE OF INVENTION:  OF INDUCING THE PRODUCTION OF INTERFERON-
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent In Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/08/884,324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: human
; TISSUE TYPE: placenta
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..3
; IDENTIFICATION METHOD: E
; NAME/KEY: leader peptide
; LOCATION: 4..82
; IDENTIFICATION METHOD: S
; NAME/KEY: intron
; LOCATION: 83..1453
; IDENTIFICATION METHOD: E
; NAME/KEY: leader peptide
; LOCATION: 1454..1465
; IDENTIFICATION METHOD: S
; NAME/KEY: intron
; LOCATION: 1466..4848
; IDENTIFICATION METHOD: E
; NAME/KEY: leader peptide
; LOCATION: 4849..4865
; IDENTIFICATION METHOD: S
; NAME/KEY: mat peptide
; LOCATION: 4866..4983
; IDENTIFICATION METHOD: S
; NAME/KEY: intron
; LOCATION: 4984..6317
; IDENTIFICATION METHOD: E
; NAME/KEY: mat peptide
; LOCATION: 6318..6451
; IDENTIFICATION METHOD: S
; NAME/KEY: intron
; LOCATION: 6452..11224
; IDENTIFICATION METHOD: E
; NAME/KEY: mat peptide
; LOCATION: 11225..11443
; IDENTIFICATION METHOD: S
; NAME/KEY: 3'UTR
; LOCATION: 11444..11464
; IDENTIFICATION METHOD: E
US-08-884-324-13

Query Match 2.0%; Score 20; DB 3; Length 11464;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 831 ACAACATCATCTCTGTTTTC 850
||||||||||||||||||||
Db 4226 ACAACATCATCTCTGTTTTC 4207

RESULT 9
US-08-884-324-14/c

; Sequence 14, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takanori OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: human
; TISSUE TYPE: placenta
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..15606
; IDENTIFICATION METHOD: E
; NAME/KEY: leader peptide
; LOCATION: 15607..15685
; IDENTIFICATION METHOD: S
; NAME/KEY: intron
; LOCATION: 15686..17056
; IDENTIFICATION METHOD: E
; NAME/KEY: leader peptide
; LOCATION: 17057..17068
; IDENTIFICATION METHOD: S
; NAME/KEY: intron
; LOCATION: 17069..20451
; IDENTIFICATION METHOD: E
; NAME/KEY: leader peptide
; LOCATION: 20452..20468
; IDENTIFICATION METHOD: S
; NAME/KEY: mat peptide
; LOCATION: 20469..20586
; IDENTIFICATION METHOD: S
; NAME/KEY: intron
; LOCATION: 20587..21920
; IDENTIFICATION METHOD: E
; NAME/KEY: mat peptide
; LOCATION: 21921..22054
; IDENTIFICATION METHOD: S

; NAME/KEY: intron
; LOCATION: 22055..26827
; IDENTIFICATION METHOD: E
; NAME/KEY: mat peptide
; LOCATION: 26828..27046
; IDENTIFICATION METHOD: S
; NAME/KEY: 3'UTR
; LOCATION: 27047..28994
; IDENTIFICATION METHOD: E
US-08-884-324-14

Query Match 2.0%; Score 20; DB 3; Length 28994;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 831 ACAACATCATCTCTGTTTTC 850
||||||||||||||||||||
Db 19829 ACAACATCATCTCTGTTTTC 19810

Search completed: October 6, 2004, 05:40:52
Job time : 102 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 5, 2004, 14:09:13 ; Search time 122 Seconds
(without alignments)
731.844 Million cell updates/sec

Title: US-10-024-444B-2
Perfect score: 316
Sequence: 1 MELRNSTLGSGFILVGILND.....VMRALRRVLGKYILLAHSTL 316

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	316	100.0	316	4	AAG71681	Aag71681 Human olf
2	316	100.0	316	5	ABB79908	Abb79908 Human olf
3	57	18.0	316	4	AAG71678	Aag71678 Human olf
4	57	18.0	316	4	AAU10317	Aau10317 G-protein
5	57	18.0	316	4	AAU24614	Aau24614 Human olf
6	57	18.0	316	4	AAU07087	Aau07087 Human odo
7	57	18.0	316	5	ABP95852	Abp95852 Human GPC
8	57	18.0	316	5	AAU95574	Aau95574 Human olf
9	57	18.0	316	5	AAU85234	Aau85234 G-coupled
10	57	18.0	316	7	ADC85823	Adc85823 Human GPC
11	57	18.0	324	4	AAU07088	Aau07088 Human odo
12	57	18.0	324	5	AAU97928	Aau97928 Novel odo
13	57	18.0	324	5	AAU97927	Aau97927 Novel odo
14	15	4.7	234	4	AAG73027	Aag73027 Olfactory
15	15	4.7	316	5	AAB71196	Aab71196 Human GPC
16	15	4.7	316	7	ADD12793	Add12793 Novel hum
17	15	4.7	338	4	AAG72714	Aag72714 Murine OR
18	14	4.4	317	4	AAG72581	Aag72581 Human OR-
19	14	4.4	317	4	AAG71586	Aag71586 Human olf
20	14	4.4	317	4	AAU24616	Aau24616 Human olf
21	14	4.4	317	5	AAE18013	Aae18013 Human G-p
22	14	4.4	317	5	AAE18012	Aae18012 Human G-p
23	14	4.4	317	5	ABB77321	Abb77321 Human G-p
24	14	4.4	317	5	ABJ03976	Abj03976 Human G-p
25	14	4.4	317	5	ABP95837	Abp95837 Human GPC
26	14	4.4	317	5	AAU95552	Aau95552 Human olf
27	14	4.4	317	5	AAU85236	Aau85236 G-coupled
28	14	4.4	317	7	ADC86213	Adc86213 Human GPC
29	13	4.1	82	4	AAB45704	Aab45704 Human 7TM
30	13	4.1	149	3	AAB41578	Aab41578 Human ORF
31	13	4.1	158	7	ADC86807	Adc86807 Human GPC
32	13	4.1	172	7	ADC86715	Adc86715 Human GPC
33	13	4.1	199	7	ADE08306	Ade08306 Novel pro
34	13	4.1	202	4	AAG71547	Aag71547 Human olf
35	13	4.1	210	4	AAG72738	Aag72738 Human olf
36	13	4.1	211	4	AAG72737	Aag72737 Human olf
37	13	4.1	212	2	AAR27879	Aar27879 Pheromone
38	13	4.1	215	4	AAG72749	Aag72749 Human olf
39	13	4.1	216	4	AAG72799	Aag72799 Human olf
40	13	4.1	216	4	AAG71988	Aag71988 Human olf
41	13	4.1	216	4	AAG72796	Aag72796 Human olf
42	13	4.1	216	4	AAG72336	Aag72336 Human OR-
43	13	4.1	216	4	AAG72842	Aag72842 Human olf
44	13	4.1	216	4	AAG72797	Aag72797 Human olf
45	13	4.1	216	4	AAG72786	Aag72786 Human olf

ALIGNMENTS

RESULT 1
AAG71681
ID AAG71681 standard; protein; 316 AA.
XX
AC AAG71681;
XX
DT 30-JUL-2001 (first entry)
XX
DE Human olfactory receptor polypeptide, SEQ ID NO: 1362.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027582.
XX
PR 08-OCT-1999; 99US-0158615P.
PR 24-FEB-2000; 2000US-0184809P.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
XX
PS Claim 11; Page 845; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by one of
CC a number of novel polynucleotides. The polynucleotides can be used in
CC screening for olfactory agonists and antagonists. The methods allow for
CC the determination of primary scents and the identification of the odour
CC receptors used to detect these primary scents. The methods also enable
CC determination of secondary scents and the identification of combinations
CC of odour receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called a
CC scent fingerprint or scent profile), which may be used to re-create and
CC edit scents. Libraries of olfactory receptors are useful for determining
CC the interaction pattern of a composition with the receptors, and can be

```
CC   used for determining differences in the olfactory faculties of different
CC   individuals
XX
SQ   Sequence 316 AA;

  Query Match             100.0%;  Score 316;  DB 4;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-281;
  Matches  316;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELRNSTLGSGFILVGILNDSGSPELLYATFTILYMLALTSNGLLLLAITIEARLHMPMY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELRNSTLGSGFILVGILNDSGSPELLYATFTILYMLALTSNGLLLLAITIEARLHMPMY 60

Qy         61 LLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMGSAEDLLLAFMAY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMGSAEDLLLAFMAY 120

Qy        121 DRYVAICHPLKYMTLMSPRVCWIMVATSWILASLIAIGHTMYTMHLPFCVSWEIRHLLCE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRYVAICHPLKYMTLMSPRVCWIMVATSWILASLIAIGHTMYTMHLPFCVSWEIRHLLCE 180

Qy        181 IPPLLKLACADTSRYELIIYVTGVTFLLLPISAIVASYTLVLFTVLRMPSNEGRKKALVT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IPPLLKLACADTSRYELIIYVTGVTFLLLPISAIVASYTLVLFTVLRMPSNEGRKKALVT 240

Qy        241 CSSHLIVVGMFYGAATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEVMRA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CSSHLIVVGMFYGAATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEVMRA 300

Qy        301 LRRVLGKYILLAHSTL 316
              ||||||||||||||||
Db        301 LRRVLGKYILLAHSTL 316


RESULT 2
ABB79908
ID   ABB79908 standard; protein; 316 AA.
XX
AC   ABB79908;
XX
DT   05-DEC-2002  (first entry)
XX
DE   Human olfactory receptor-like protein GPCR1.
XX
KW   GPCR1; olfactory receptor; G-protein coupled receptor; receptor; human;
KW   antiarteriosclerotic; antidiabetic; analgesic; cytostatic;
KW   antidepressant; nootropic; neuroprotective; immunosuppressive;
KW   antiallergic; antibacterial; virucide; protozoacide; fungicide;
KW   cardiomyopathy; atherosclerosis; diabetes; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          41. .290
FT                   /note= "7tm_1 domain"
XX
PN   WO200270707-A2.
XX
PD   12-SEP-2002.
XX
PF   18-DEC-2001; 2001WO-US049168.
XX
PR   18-DEC-2000; 2000US-0256635P.
XX
PA   (CURA-) CURAGEN CORP.
PA   (CORT-) COR THERAPEUTICS INC.
XX
PI   Padigaru M,  Gerlach VL,  Smithson G,  Stone D,  Bin-Yang R;
PI   Conley P,  Hart M,  Tomlinson JE,  Topper JN,  Kekuda R,  Casman SJ;
PI   Edinger S,  Macdougall JR;
XX
DR   WPI; 2002-698753/75.
DR   N-PSDB; ABQ81238.
XX
PT   New G-protein coupled receptor (GPCR1) proteins and nucleic acids, useful
PT   for treating or preventing a GPCR1-associated disorder, e.g.
PT   cardiomyopathy, atherosclerosis, diabetes, or disorders related to cell
PT   signal processing.
XX
PS   Claim 1; Page 11; 111pp; English.
XX
CC   The present sequence is the protein sequence of a novel human G-protein
CC   coupled receptor, designated GPCR1, that has structural and physiological
CC   functions characteristic of the olfactory receptor family, and has
CC   properties similar to those of proteins containing the 7tm_1 7
CC   transmembrane receptor (rhodopsin family). The invention provides GPCR1
CC   polypeptides and nucleic acids, and methods for their recombinant
CC   production. These are useful for treating or preventing a GPCR1-
CC   associated disorder, such as cardiomyopathy, atherosclerosis, diabetes,
CC   or a disorder related to cell signal processing or metabolic pathway
CC   modulation in humans (claimed). They may further be used for treating or
CC   preventing e.g. developmental diseases, metabolic pathway disorders,
CC   retinal disorders, wasting disorders associated with chronic diseases,
CC   pain, cancer, psychotic and neurological disorders (e.g. anxiety or
CC   schizophrenia), autoimmune diseases, allergies, bacterial, fungal,
CC   protozoal and viral infections, neurodegenerative diseases (e.g.
CC   Alzheimer's disease), and haematopoietic diseases. The proteins and
CC   nucleic acids may also be used as research tools, as diagnostic or
CC   prognostic markers, in gene therapy, for promoting tissue regeneration in
CC   vitro and in vivo, and as biological defence weapons. The proteins are
CC   also are useful for producing antibodies specific for the proteins, as
CC   vaccines, and in screening for potential agonists and antagonists
XX
SQ   Sequence 316 AA;

  Query Match             100.0%;  Score 316;  DB 5;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-281;
  Matches  316;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELRNSTLGSGFILVGILNDSGSPELLYATFTILYMLALTSNGLLLLAITIEARLHMPMY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELRNSTLGSGFILVGILNDSGSPELLYATFTILYMLALTSNGLLLLAITIEARLHMPMY 60

Qy         61 LLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMGSAEDLLLAFMAY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMGSAEDLLLAFMAY 120

Qy        121 DRYVAICHPLKYMTLMSPRVCWIMVATSWILASLIAIGHTMYTMHLPFCVSWEIRHLLCE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRYVAICHPLKYMTLMSPRVCWIMVATSWILASLIAIGHTMYTMHLPFCVSWEIRHLLCE 180

Qy        181 IPPLLKLACADTSRYELIIYVTGVTFLLLPISAIVASYTLVLFTVLRMPSNEGRKKALVT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IPPLLKLACADTSRYELIIYVTGVTFLLLPISAIVASYTLVLFTVLRMPSNEGRKKALVT 240

Qy        241 CSSHLIVVGMFYGAATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEVMRA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CSSHLIVVGMFYGAATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEVMRA 300

Qy        301 LRRVLGKYILLAHSTL 316
              ||||||||||||||||
Db        301 LRRVLGKYILLAHSTL 316


RESULT 3
AAG71678
ID   AAG71678 standard; protein; 316 AA.
XX
AC   AAG71678;
XX
DT   30-JUL-2001  (first entry)
XX
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1359.
XX
KW   Human; olfactory receptor; OR; primary scent determination;
KW   secondary scent determination; polypeptide library; odour receptor;
```

KW scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027582.
XX
PR 08-OCT-1999; 99US-0158615P.
PR 24-FEB-2000; 2000US-0184809P.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
XX
PS Claim 11; Page 842-843; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by one of
CC a number of novel polynucleotides. The polynucleotides can be used in
CC screening for olfactory agonists and antagonists. The methods allow for
CC the determination of primary scents and the identification of the odour
CC receptors used to detect these primary scents. The methods also enable
CC determination of secondary scents and the identification of combinations
CC of odour receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called a
CC scent fingerprint or scent profile), which may be used to re-create and
CC edit scents. Libraries of olfactory receptors are useful for determining
CC the interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
CC individuals
XX
SQ Sequence 316 AA;

Query Match 18.0%; Score 57; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 4
AAU10317
ID AAU10317 standard; protein; 316 AA.
XX
AC AAU10317;
XX
DT 25-JAN-2002 (first entry)
XX
DE G-protein coupled receptor (GCREC) #18.
XX
KW G-protein coupled receptor; GCREC; vaccine; gene therapy;
KW cell proliferation disorder; cancer; arteriosclerosis;
KW neurological disorder; epilepsy; stroke; cardiovascular disorder;
KW hypertension; ischaemic heart disease; gastrointestinal disorder;
KW anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
KW diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
KW schizophrenic disorder; neuroskeletal disorder.
XX
OS Homo sapiens.
XX
PN WO200166742-A2.
XX
PD 13-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US006814.
XX
PR 03-MAR-2000; 2000US-0186854P.
PR 10-MAR-2000; 2000US-0188384P.
PR 17-MAR-2000; 2000US-0190453P.
PR 20-MAR-2000; 2000US-0190730P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM;
PI Lu DAM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J, Harland L;
PI Walsh RT, Lo TP, Borowsky ML;
XX
DR WPI; 2001-656776/75.
DR N-PSDB; AAS15914.
XX
PT Novel G-protein coupled receptor polypeptides, for treating and
PT preventing autoimmune/inflammatory disorders, neurological disorders,
PT cell proliferative disorders, cardiovascular disorders and viral
PT infections.
XX
PS Claim 1; Page 128; 141pp; English.
XX
CC The invention describes a novel isolated polypeptide, selected from a
CC group of 21 G-protein coupled receptor polypeptides (GCREC) and useful in
CC vaccines and gene therapy. The polypeptide (I) is useful for screening
CC for agonist or antagonist of (I), compounds specifically binding to (I),
CC or compounds that modulate the activity of (I). The polynucleotide
CC encoding (1) is useful for screening a compound for effectiveness in
CC altering expression of a target polynucleotide comprising (II), by
CC exposing a sample comprising the target polynucleotide to a compound,
CC detecting altered expression of the target polynucleotide, and comparing
CC the expression of the target polynucleotide in the presence of varying
CC amounts of compound and in the absence of the compound. (I) and (II) are
CC useful for diagnosis, treatment and prevention of cell proliferative
CC disorders (e.g. cancers, arteriosclerosis, atherosclerosis), neurological
CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and
CC neuroskeletal disorders), cardiovascular disorders (e.g. hypertension,
CC ischaemic heart disease), gastrointestinal disorders (e.g. anorexia,
CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,
CC osteoporosis, psoriasis), and metabolic disorders such as obesity.
CC Furthermore, the polynucleotide is useful; as primers for detecting
CC single nucleotide polymorphisms; as elements in microarray, to monitor or
CC measure protein-protein interactions, drug-target interactions, and gene
CC expression profiles; to generate a transcript image of a tissue or cell
CC type, and to generate hybridisation probes useful in mapping the
CC naturally occurring genomic sequence. This is the G-protein coupled
CC receptor 18 (GCREC-18), one of 21 GCREC proteins described in the method
CC of the invention
XX
SQ Sequence 316 AA;

Query Match 18.0%; Score 57; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 5
AAU24614
ID AAU24614 standard; protein; 316 AA.
XX
AC AAU24614;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human olfactory receptor AOLFR107.
XX
KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;

KW food additive; cosmetic; fragrance; pharmaceutical additive.
XX
OS Homo sapiens.
XX
PN WO200168805-A2.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US007771.
XX
PR 13-MAR-2000; 2000US-0188914P.
PR 24-MAR-2000; 2000US-0192033P.
PR 12-APR-2000; 2000US-0198474P.
PR 24-APR-2000; 2000US-0199335P.
PR 26-MAY-2000; 2000US-0207702P.
PR 23-JUN-2000; 2000US-0213849P.
PR 16-AUG-2000; 2000US-0226534P.
PR 07-SEP-2000; 2000US-0230732P.
PR 07-FEB-2001; 2001US-0266862P.
XX
PA (SENO-) SENOMYX INC.
XX
PI Zozulya S;
XX
DR WPI; 2001-570867/64.
DR N-PSDB; AAS42307.
XX
PT Nucleic acids encoding human olfactory G protein-coupled receptors,
PT useful for screening for compounds involved in olfactory sensation, where
PT the compounds can be used in the food, pharmaceutical and cosmetic
PT industries to customize odors.
XX
PS Claim 60; Page 127; 319pp; English.
XX
CC The invention relates to nucleic acids encoding human olfactory
CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
CC specifically recognise molecules, odourants, that elicit specific
CC olfactory sensation. The human olfactory receptors and polynucleotides
CC encoding them are useful for screening a library of chemical compounds
CC for compounds that are involved in olfactory sensation. Modulators of
CC their activity are useful for pharmacological and genetic modulation of
CC olfactory signalling pathways. Therefore, they can be used in the food,
CC pharmaceutical and cosmetic industries to customise odours and
CC fragrances. The present sequence is a human olfactory receptor of the
CC invention
XX
SQ Sequence 316 AA;

Query Match 18.0%; Score 57; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 6
AAU07087
ID AAU07087 standard; protein; 316 AA.
XX
AC AAU07087;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human odorant receptor (OR) polypeptide #4.
XX
KW Human; olfactory receptor; OR; G-protein coupled receptor superfamily;
KW GPCR; gene therapy; tranquiliser; vulnerary; anti-HIV; cytostatic;
KW nootropic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;
KW antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
KW human immunodeficiency virus; neoplastic growth; neurological disorder;
KW Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
KW wound healing; asthma; Albright hereditary osteodystrophy;
KW multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
XX
OS Homo sapiens.
XX
PN WO200157215-A2.
XX
PD 09-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003923.
XX
PR 07-FEB-2000; 2000US-0180511P.
PR 07-FEB-2000; 2000US-0180630P.
PR 07-FEB-2000; 2000US-0180646P.
PR 08-FEB-2000; 2000US-0180930P.
PR 08-FEB-2000; 2000US-0181004P.
PR 08-FEB-2000; 2000US-0181013P.
PR 08-FEB-2000; 2000US-0181043P.
PR 24-JUL-2000; 2000US-0220262P.
PR 25-JUL-2000; 2000US-0220594P.
PR 11-AUG-2000; 2000US-0224596P.
PR 02-NOV-2000; 2000US-0245292P.
PR 06-FEB-2001; 2001US-00777789.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS;
PI Baumgartner JC;
XX
DR WPI; 2001-488883/53.
DR N-PSDB; AAS11687.
XX
PT Novel isolated NOVX polypeptide related to human odorant receptor family
PT of G-protein coupled receptor superfamily of proteins useful for treating
PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
XX
PS Claim 1; Page 39; 199pp; English.
XX
CC Novel isolated NOVX polynucleotides and their encoded polypeptides of the
CC invention are related to the human olfactory (or odorant) receptors
CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
CC sequences are useful for treating or preventing a pathology associated
CC with OR in a subject, and for manufacturing a medicament for treating a
CC syndrome associated with a human disease. These diseases include
CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
CC growth, neurological disorders, such as Parkinson's disease and
CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
CC disease, multiple sclerosis, and Albright hereditary osteodystrophy. The
CC polynucleotides and polypeptides are also useful, to identify proteins of
CC the same family, to screen for molecules which inhibit or enhance the
CC activity or function of olfactory receptors, to detect nasal epithelial
CC neuronal tissue, in production of transgenic plants and for the
CC development of new drug targets for various disorders. This sequence
CC represents a human OR polypeptide
XX
SQ Sequence 316 AA;

Query Match 18.0%; Score 57; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 7
ABP95852
ID ABP95852 standard; protein; 316 AA.
XX
AC ABP95852;
XX
DT 06-MAR-2003 (first entry)

XX
DE Human GPCR polypeptide SEQ ID NO 514.
XX
KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; receptor.
XX
OS Homo sapiens.
XX
PN WO200216548-A2.
XX
PD 28-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-IB001446.
XX
PR 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Haga T, Takeda S, Mitaku S;
XX
DR WPI; 2002-304118/34.
DR N-PSDB; ABZ43126.
XX
PT Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
XX
PS Claim 10; SEQ ID NO 514; 97pp + Sequence Listing; Japanese.
XX
CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 316 AA;

Query Match 18.0%; Score 57; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 8
AAU95574
ID AAU95574 standard; protein; 316 AA.
XX
AC AAU95574;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human olfactory and pheromone G protein-coupled receptor #61.
XX
KW Human; olfactory and pheromone G protein coupled; receptor; GPCR;
KW tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
KW anorectic; taste; fragrance; food additive; cosmetic; cell migration;
KW sterility; psychotic disorder; neurological disorder; anxiety;
KW schizophrenia; manic depression; depression; axonal growth;
KW menstrual cycle; appetite sexual motivation; sexual attraction;
KW aggression.
XX
OS Homo sapiens.
XX
PN WO200224726-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-BE000162.
XX
PR 22-SEP-2000; 2000EP-00870211.
XX
PA (CHEM-) CHEMCOM SA.
XX
PI Veithen A;
XX
DR WPI; 2002-330013/36.
DR N-PSDB; ABK68461.
XX
PT Novel pheromone G-protein coupled receptor and receptor-derived agonists,
PT antagonists or inhibitors useful in food or cosmetic products or in the
PT treatment or prevention of neurological disorders such as anxiety and
PT schizophrenia.
XX
PS Disclosure; Page 197-198; 833pp; English.
XX
CC The invention relates to olfactory and Pheromone G-protein coupled
CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
CC portion and its encoding polynucleotide. Also included are an agonist,
CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector
CC comprising the polynucleotide, a cell transformed by the vector, a non-
CC human mammal comprising a partial or total deletion of the polynucleotide
CC encoding the receptor and screening (detection and possibly, recovering)
CC of compounds which are known or not known to be agonist, antagonists or
CC inhibitors of natural compounds to the GPCR. The receptor-derived
CC agonists, antagonists, inhibitors or compounds are used as an
CC improvement, elimination or substitution of an existing taste and/or a
CC fragrance of (or in) the food and/or cosmetic products. They can also be
CC used in the preparation of medicament in the treatment and/or prevention
CC of a mammalian disorder, such as cell migration, sterility, psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, depression, for promoting axonal growth, nerve cell
CC connection and nerve regeneration for modulating male and female
CC endocrine functions, hormone production and the menstrual cycle, for the
CC prevention or the treatment by stimulation of several mammalian
CC behaviours, such as stimulation or suppression of appetite, sexual
CC motivation, sexual attraction, aggression and for promoting or
CC suppressing chemical communication between organisms. The present
CC sequence is a human olfactory and pheromone GPCR protein sequence
XX
SQ Sequence 316 AA;

Query Match 18.0%; Score 57; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 9
AAU85234
ID AAU85234 standard; protein; 316 AA.
XX
AC AAU85234;
XX
DT 08-MAY-2002 (first entry)
XX
DE G-coupled olfactory receptor #95.
XX
KW Human; olfactory G-coupled receptor; sensory perception of odourant;
KW odour composition; taste composition.
XX
OS Homo sapiens.
XX

PN WO200198526-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020122.
XX
PR 22-JUN-2000; 2000US-0213812P.
PR 13-MAR-2001; 2001US-00804291.
XX
PA (SENO-) SENOMYX INC.
XX
PI Zozulya S, Stryer L;
XX
DR WPI; 2002-083330/11.
DR N-PSDB; ABK37593.
XX
PT Representing sensory perception of one or more odorants for the
PT identification and design of tastes and odors comprises providing a
PT representative group of n olfactory receptors.
XX
PS Claim 1; Page 101; 182pp; English.
XX
CC The invention relates to a method of representing sensory perception of
CC one or more odourants. The method comprises: (a) providing a
CC representative class of n olfactory receptors or ligand binding domains
CC (LBD) of these receptors; (b) measuring values X1 to Xn representative of
CC at least one activity of one or more odourants selected from: (i) binding
CC one or more odourants to the LBD of at least one of the n olfactory
CC receptors; (ii) activating at least one of the n olfactory receptors with
CC the one or more odourants; and (iii) blocking at least one of the n
CC olfactory receptors with the one or more odourants; and (c) generating a
CC representation of sensory perception from the values X1 to Xn. The
CC representation of the sensory perception of odourants is useful for the
CC design and formulation of odour and taste compositions. AAU85140-AAU85393
CC represent human olfactory G-coupled receptor amino acid sequences of the
CC invention
XX
SQ Sequence 316 AA;

Query Match 18.0%; Score 57; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 10
ADC85823
ID ADC85823 standard; protein; 316 AA.
XX
AC ADC85823;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR protein SEQ ID NO:276.
XX
KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
DR WPI; 2003-315783/31.
DR N-PSDB; ADC85822.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 2; SEQ ID NO 276; 28pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
SQ Sequence 316 AA;

Query Match 18.0%; Score 57; DB 7; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.3e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108

RESULT 11
AAU07088
ID AAU07088 standard; protein; 324 AA.
XX
AC AAU07088;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human odorant receptor (OR) polypeptide #5.
XX
KW Human; olfactory receptor; OR; G-protein coupled receptor superfamily;
KW GPCR; gene therapy; tranquiliser; vulnerary; anti-HIV; cytostatic;
KW nootropic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;
KW antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
KW human immunodeficiency virus; neoplastic growth; neurological disorder;
KW Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
KW wound healing; asthma; Albright hereditary osteodystrophy;
KW multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
XX
OS Homo sapiens.
XX
PN WO200157215-A2.
XX
PD 09-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003923.
XX
PR 07-FEB-2000; 2000US-0180511P.
PR 07-FEB-2000; 2000US-0180630P.
PR 07-FEB-2000; 2000US-0180646P.
PR 08-FEB-2000; 2000US-0180930P.
PR 08-FEB-2000; 2000US-0181004P.
PR 08-FEB-2000; 2000US-0181013P.
PR 08-FEB-2000; 2000US-0181043P.
PR 24-JUL-2000; 2000US-0220262P.
PR 25-JUL-2000; 2000US-0220594P.
PR 11-AUG-2000; 2000US-0224596P.
PR 02-NOV-2000; 2000US-0245292P.
PR 06-FEB-2001; 2001US-00777789.
XX
PA (CURA-) CURAGEN CORP.
XX

PI Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS;
PI Baumgartner JC;
XX
DR WPI; 2001-488883/53.
DR N-PSDB; AAS11688.
XX
PT Novel isolated NOVX polypeptide related to human odorant receptor family
PT of G-protein coupled receptor superfamily of proteins useful for treating
PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
XX
PS Claim 1; Page 44; 199pp; English.
XX
CC Novel isolated NOVX polynucleotides and their encoded polypeptides of the
CC invention are related to the human olfactory (or odorant) receptors
CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
CC sequences are useful for treating or preventing a pathology associated
CC with OR in a subject, and for manufacturing a medicament for treating a
CC syndrome associated with a human disease. These diseases include
CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
CC growth, neurological disorders, such as Parkinson's disease and
CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
CC disease, multiple sclerosis, and Albright hereditary osteodystrophy. The
CC polynucleotides and polypeptides are also useful, to identify proteins of
CC the same family, to screen for molecules which inhibit or enhance the
CC activity or function of olfactory receptors, to detect nasal epithelial
CC neuronal tissue, in production of transgenic plants and for the
CC development of new drug targets for various disorders. This sequence
CC represents a human OR polypeptide
XX
SQ Sequence 324 AA;

Query Match 18.0%; Score 57; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 9.5e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 60 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 116

RESULT 12
AAU97928
ID AAU97928 standard; protein; 324 AA.
XX
AC AAU97928;
XX
DT 15-AUG-2002 (first entry)
XX
DE Novel odourant receptor NOV7 protein.
XX
KW NOV; odorant receptor; G protein coupled receptor; GPCR; trauma;
KW olfactory receptor; olfactory loss; neoplastic growth;
KW human immunodeficiency virus; Alzheimer's disease; HIV;
KW neurological disorder; Parkinson's disease.
XX
OS Unidentified.
XX
PN WO200236632-A2.
XX
PD 10-MAY-2002.
XX
PF 09-OCT-2001; 2001WO-US031744.
XX
PR 02-NOV-2000; 2000US-0245292P.
PR 06-FEB-2001; 2001US-00777789.
PR 20-SEP-2001; 2001US-00245292.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Burgess CE, Grosse WM, Lepley DM, Padigaru M;
PI Spytek KA;
XX
DR WPI; 2002-471499/50.
DR N-PSDB; ABK53097.
XX
PT New isolated olfactory receptor-like polypeptide, NOVX, useful for
PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
PT trauma, human immunodeficiency virus illness, neoplastic growth and
PT neurological disorders.
XX
PS Claim 1; Page 34-35; 122pp; English.
XX
CC This invention relates to the DNA and protein sequences of a novel
CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
CC sequences of the invention and an antibody specific for the protein are
CC useful for treating or preventing a disorder associated with NOV1 in a
CC subject, preferably human. A NOVX specific antibody is useful for
CC determining the presence or amount of protein in a sample. The DNA,
CC protein and antibody of the invention is useful for diagnosing,
CC preventing or treating disorders associated with aberrant NOVX expression
CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
CC antibody is useful in screening assays, detection assays (e.g.,
CC chromosomal mapping, tissue typing, forensic biology), predictive
CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
CC trials and pharmacogenomic), and in methods of treatment (e.g.,
CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC produce antibodies immunospecific for the protein, to screen for
CC potential agonist and antagonist compounds, and as bait protein in a two-
CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
CC invention is useful for isolating, and purifying the protein and to
CC monitor protein levels in tissue as part of a clinical testing procedure.
CC The present sequence represents the NOV7 protein of the invention
XX
SQ Sequence 324 AA;

Query Match 18.0%; Score 57; DB 5; Length 324;
Best Local Similarity 100.0%; Pred. No. 9.5e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 60 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 116

RESULT 13
AAU97927
ID AAU97927 standard; protein; 324 AA.
XX
AC AAU97927;
XX
DT 15-AUG-2002 (first entry)
XX
DE Novel odourant receptor NOV6 protein.
XX
KW NOV; odorant receptor; G protein coupled receptor; GPCR; trauma;
KW olfactory receptor; olfactory loss; neoplastic growth;
KW human immunodeficiency virus; Alzheimer's disease; HIV;
KW neurological disorder; Parkinson's disease.
XX
OS Unidentified.
XX
PN WO200236632-A2.
XX
PD 10-MAY-2002.
XX
PF 09-OCT-2001; 2001WO-US031744.
XX
PR 02-NOV-2000; 2000US-0245292P.
PR 06-FEB-2001; 2001US-00777789.
PR 20-SEP-2001; 2001US-00245292.
XX
PA (CURA-) CURAGEN CORP.

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XX
PI   Alsobrook JP,  Burgess CE,  Grosse WM,  Lepley DM,  Padigaru M;
PI   Spytek KA;
XX
DR   WPI; 2002-471499/50.
DR   N-PSDB; ABK53096.
XX
PT   New isolated olfactory receptor-like polypeptide, NOVX, useful for
PT   diagnosing, preventing or treating disorders of olfactory loss, e.g.
PT   trauma, human immunodeficiency virus illness, neoplastic growth and
PT   neurological disorders.
XX
PS   Claim 1; Page 33; 122pp; English.
XX
CC   This invention relates to the DNA and protein sequences of a novel
CC   isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
CC   sequences of the invention and an antibody specific for the protein are
CC   useful for treating or preventing a disorder associated with NOV1 in a
CC   subject, preferably human. A NOVX specific antibody is useful for
CC   determining the presence or amount of protein in a sample. The DNA,
CC   protein and antibody of the invention is useful for diagnosing,
CC   preventing or treating disorders associated with aberrant NOVX expression
CC   such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
CC   virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
CC   Parkinson's disease and Alzheimer's disease. The sequences and NOV
CC   antibody is useful in screening assays, detection assays (e.g.,
CC   chromosomal mapping, tissue typing, forensic biology), predictive
CC   medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
CC   trials and pharmacogenomic), and in methods of treatment (e.g.,
CC   therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC   produce antibodies immunospecific for the protein, to screen for
CC   potential agonist and antagonist compounds, and as bait protein in a two-
CC   hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC   therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
CC   in a NOVX gene, and to modulate NOVX activity. The antibody of the
CC   invention is useful for isolating, and purifying the protein and to
CC   monitor protein levels in tissue as part of a clinical testing procedure.
CC   The present sequence represents the NOV6 protein of the invention
XX
SQ   Sequence 324 AA;

  Query Match             18.0%;  Score 57;  DB 5;  Length 324;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-44;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 116


RESULT 14
AAG73027
ID   AAG73027 standard; protein; 234 AA.
XX
AC   AAG73027;
XX
DT   30-JUL-2001  (first entry)
XX
DE   Olfactory receptor-like polypeptide, SEQ ID NO: 2709.
XX
KW   Human; olfactory receptor; OR; primary scent determination;
KW   secondary scent determination; polypeptide library; odour receptor;
KW   scent profile; scent fingerprint; scent representation.
XX
OS   Unidentified.
XX
PN   WO200127158-A2.
XX
PD   19-APR-2001.
XX
PF   06-OCT-2000; 2000WO-US027582.
XX
PR   08-OCT-1999;    99US-0158615P.
PR   24-FEB-2000; 2000US-0184809P.
XX
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Bellenson J,  Smith D,  Lancet D,  Glusman G,  Fuchs T,  Yanai I;
XX
DR   WPI; 2001-290713/30.
XX
PT   New polynucleotides which encode polypeptides involved in olfactory
PT   sensation for identifying olfactory agonists and antagonists.
XX
PS   Example 6; Page 1832-1833; 1857pp; English.
XX
CC   The present sequence is an olfactory receptor polypeptide which was used
CC   as a query sequence in a database search of olfactory receptor (OR)-like
CC   sequences. The invention relates to isolated polynucleotides encoding
CC   polypeptides involved in olfactory sensation. The polynucleotides can be
CC   used in screening for olfactory agonists and antagonists. The methods
CC   allow for the determination of primary scents and the identification of
CC   the odour receptors used to detect these primary scents. The methods also
CC   enable determination of secondary scents and the identification of
CC   combinations of odour receptors that are involved in detecting such
CC   secondary scents. This enables the construction of a scent representation
CC   (also called a scent fingerprint or scent profile), which may be used to
CC   re-create and edit scents. Libraries of olfactory receptors are useful
CC   for determining the interaction pattern of a composition with the
CC   receptors, and can be used for determining differences in the olfactory
CC   faculties of different individuals
XX
SQ   Sequence 234 AA;

  Query Match             4.7%;  Score 15;  DB 4;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPLKY 132
              |||||||||||||||
Db         60 MAYDRYVAICHPLKY 74


RESULT 15
AAB71196
ID   AAB71196 standard; protein; 316 AA.
XX
AC   AAB71196;
XX
DT   12-NOV-2002  (first entry)
XX
DE   Human GPCRX protein SEQ ID 68.
XX
KW   Human; anti-HIV; nootropic; antiasthmatic; antiarteriosclerotic; GPCRX;
KW   immunosuppressive; immunomodulator; cytostatic; antiinflammatory; AIDS;
KW   antidiabetic; neuroprotective; anorectic; haemostatic; antibacterial;
KW   fungicide; protozoal; virucide; human G-protein coupled receptor;
KW   gene therapy; vaccine; cardiomyopathy; atherosclerosis; diabetes;
KW   cell signal processing; cancer; obesity; neurodegenerative disorder;
KW   cachexia; anorexia; Alzheimer's disease; Parkinson's disease;
KW   immune disorder; graft versus host disease; bronchial asthma;
KW   Crohn's disease; multiple sclerosis; haemophilia; infectious disease;
KW   idiopathic thrombocytopenic purpura; receptor.
XX
OS   Homo sapiens.
XX
PN   WO200250275-A2.
XX
PD   27-JUN-2002.
XX
PF   18-DEC-2001; 2001WO-US048958.
XX
PR   18-DEC-2000; 2000US-0256635P.
PR   21-DEC-2000; 2000US-0257876P.
PR   04-JAN-2001; 2001US-0259743P.
```

PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Kekuda R, Li L, Ballinger RA, Casman SJ, Spytek KA;
PI Baumgartner JC, Burgess CE;
XX
DR WPI; 2002-657419/70.
DR N-PSDB; AAF88435.
XX
PT New G-protein coupled receptor polypeptides, useful in gene therapy,
PT particularly for treating or preventing cardiomyopathy, atherosclerosis,
PT diabetes, Crohn's disease, hemophilia or cancer in humans.
XX
PS Claim 1; Page 112; 155pp; English.
XX
CC This invention describes novel human G-protein coupled receptor (GPCRX)
CC polypeptides which have anti-HIV, nootropic, antiasthmatic, protozoal;
CC antiarteriosclerotic; immunosuppressive, immunomodulator, cytostatic,
CC antiinflammatory, antidiabetic, neuroprotective, anorectic, haemostatic,
CC antibacterial, fungicide and virucide activity. The products of the
CC invention can be used in gene therapy or for vaccines. The GPCRX
CC polypeptide, GPCRX nucleic acid and antibody are useful for treating,
CC preventing or alleviating a GPCRX-associated disorder or a pathological
CC state in a subject e.g cardiomyopathy, atherosclerosis, diabetes, or a
CC disorder related to cell signal processing and metabolic pathway
CC modulation. The GPCRX polypeptide and nucleic acid are also useful for
CC diagnosing the presence of or predisposition to a disease associated with
CC altered levels of GPCRX, particularly cancer. These polypeptides, nucleic
CC acids and antibodies are also useful for treating or preventing obesity,
CC neurodegenerative disorders, AIDS, cancer-associated cachexia, anorexia,
CC Alzheimer's disease, Parkinson's disease, immune disorders, graft versus
CC host disease, bronchial asthma, Crohn's disease, multiple sclerosis,
CC haemophilia, idiopathic thrombocytopenic purpura or infectious disease.
CC They can also be used to screen for potential agonist and antagonist
CC compounds. The polypeptides are also useful as immunogens to produce
CC antibodies or as vaccines. Anti-GPCRX antibodies can be used
CC diagnostically to monitor protein levels in tissue as part of a clinical
CC testing procedure such as in determining the efficacy of a given
CC treatment regimen. The host cells are useful in producing non-human
CC transgenic animals which are useful for studying the function and/or
CC activity of GPCRX protein and for identifying and/or evaluating
CC modulators of GPCRX protein activity. AAB71163-AAB71226 represent the
CC human GPCRX proteins encoded by AAF88402-AAF88465
XX
SQ Sequence 316 AA;

Query Match 4.7%; Score 15; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      118 MAYDRYVAICHPLKY 132
            |||||||||||||||
Db      124 MAYDRYVAICHPLKY 138
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Search completed: October 5, 2004, 14:21:37
Job time : 127 secs

OM protein - protein search, using sw model

Run on: October 5, 2004, 14:18:09 ; Search time 40 Seconds (without alignments) 759.913 Million cell updates/sec

Title: US-10-024-444B-2
Perfect score: 316
Sequence: 1 MELRNSTLGSGFILVGILND.....VMRALRRVLGKYILLAHSTL 316

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	4.7	234	2	S28999	G protein-coupled
2	13	4.1	232	2	S29001	G protein-coupled
3	13	4.1	311	2	JC5200	chemoreceptor TB33
4	13	4.1	315	2	JC5201	chemoreceptor TB56
5	13	4.1	327	2	F23701	olfactory receptor
6	12	3.8	333	2	A23701	olfactory receptor
7	11	3.5	222	2	D40745	odorant receptor (
8	11	3.5	304	2	S29709	olfactory receptor
9	11	3.5	309	1	S51356	olfactory receptor
10	10	3.2	165	2	I38471	olfactory receptor
11	10	3.2	168	2	S28997	G protein-coupled
12	10	3.2	215	2	I38473	olfactory receptor
13	10	3.2	216	2	I38470	olfactory receptor
14	10	3.2	216	2	I38474	olfactory receptor
15	10	3.2	222	2	C40745	odorant receptor (
16	10	3.2	222	2	B40745	odorant receptor (
17	10	3.2	225	2	I38478	olfactory receptor
18	10	3.2	307	2	S29710	olfactory receptor
19	10	3.2	310	2	E23701	olfactory receptor
20	10	3.2	312	2	A46750	olfactory receptor
21	10	3.2	312	2	A48413	probable olfactory
22	10	3.2	312	2	G23701	olfactory receptor
23	10	3.2	312	2	S29708	olfactory receptor
24	10	3.2	312	2	I23701	olfactory receptor
25	10	3.2	313	2	S20571	olfactory receptor
26	10	3.2	314	2	S20572	olfactory receptor
27	10	3.2	314	2	H23701	olfactory receptor
28	10	3.2	314	2	S29707	olfactory receptor
29	10	3.2	314	2	A37286	olfactory receptor
30	9	2.8	157	2	S58073	probable olfactory
31	9	2.8	315	2	JC5836	olfactory receptor
32	9	2.8	367	2	I49022	kappa opioid recep
33	9	2.8	367	2	JC2421	opioid receptor ho
34	9	2.8	367	2	I56520	G protein-coupled
35	9	2.8	370	2	S43087	orphan opioid rece
36	9	2.8	370	2	AG3073	hypothetical prote
37	9	2.8	370	2	B98213	probable maltose/m
38	8	2.5	147	2	AI3157	hypothetical prote
39	8	2.5	157	2	S58000	probable olfactory
40	8	2.5	157	2	S58029	probable olfactory
41	8	2.5	157	2	S58037	probable olfactory
42	8	2.5	168	2	G95023	acetyltransferase,
43	8	2.5	168	2	H97894	hypothetical prote
44	8	2.5	171	2	B71147	hypothetical prote
45	8	2.5	180	2	E97200	probable phosphata

ALIGNMENTS

RESULT 1
S28999
G protein-coupled receptor (clone PTE38) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C;Accession: S28999
R;Abe, K.; Kusakabe, Y.; Tanemura, K.; Emori, Y.; Arai, S.
FEBS Lett. 316, 253-256, 1993
A;Title: Multiple genes for G protein-coupled receptors and their expression in lingual
A;Reference number: S28996; MUID:93138133; PMID:8380780
A;Accession: S28999
A;Molecule type: mRNA
A;Residues: 1-234 <ABE>
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 4.7%; Score 15; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 9.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAICHPLKY 132
||||||||||||||| :
Db 60 MAYDRYVAICHPLKY 74

RESULT 2
S29001
G protein-coupled receptor (clone PTE58) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C;Accession: S29001
R;Abe, K.; Kusakabe, Y.; Tanemura, K.; Emori, Y.; Arai, S.
FEBS Lett. 316, 253-256, 1993
A;Title: Multiple genes for G protein-coupled receptors and their expression in lingual e
A;Reference number: S28996; MUID:93138133; PMID:8380780
A;Accession: S29001
A;Molecule type: mRNA
A;Residues: 1-232 <ABE>
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 4.1%; Score 13; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAICHPL 130
||||||||||||| :
Db 58 MAYDRYVAICHPL 70

RESULT 3
JC5200

chemoreceptor TB334 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
C;Accession: JC5200; PC4302
R;Thomas, M.B.; Haines, S.L.; Akeson, R.A.
Gene 178, 1-5, 1996
A;Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.
A;Reference number: JC5200; MUID:97080538; PMID:8921883
A;Accession: JC5200
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-311 <THO1>
A;Cross-references: GB:U50947; NID:g1256388; PIDN:AAC52909.1; PID:g1256389
A;Accession: PC4302
A;Status: preliminary
A;Molecule type: protein
A;Residues: 146-153;265-272 <THO2>
A;Experimental source: taste bud
C;Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
C;Genetics:
A;Gene: tb334
C;Superfamily: olfactory receptor OR14
C;Keywords: olfaction; taste bud; transmembrane protein
F;24-47/Domain: transmembrane #status predicted <TM1>
F;56-77/Domain: transmembrane #status predicted <TM2>
F;99-118/Domain: transmembrane #status predicted <TM3>
F;138-162/Domain: transmembrane #status predicted <TM4>
F;195-217/Domain: transmembrane #status predicted <TM5>
F;236-258/Domain: transmembrane #status predicted <TM6>
F;271-291/Domain: transmembrane #status predicted <TM7>

Query Match 4.1%; Score 13; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAICHPL 130
||||||||||||
Db 116 MAYDRYVAICHPL 128

RESULT 4
JC5201
chemoreceptor TB567 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
C;Accession: JC5201; PC4303
R;Thomas, M.B.; Haines, S.L.; Akeson, R.A.
Gene 178, 1-5, 1996
A;Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.
A;Reference number: JC5200; MUID:97080538; PMID:8921883
A;Accession: JC5201
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-315 <THO1>
A;Cross-references: GB:U50948; NID:g1256390; PIDN:AAC52910.1; PID:g1256391
A;Accession: PC4303
A;Status: preliminary
A;Molecule type: protein
A;Residues: 144-151;270-277 <THO2>
A;Experimental source: taste bud
C;Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
C;Genetics:
A;Gene: tb567
C;Superfamily: olfactory receptor OR14
C;Keywords: olfaction; taste bud; transmembrane protein
F;26-49/Domain: transmembrane #status predicted <TM1>
F;58-79/Domain: transmembrane #status predicted <TM2>
F;101-120/Domain: transmembrane #status predicted <TM3>
F;140-164/Domain: transmembrane #status predicted <TM4>
F;197-219/Domain: transmembrane #status predicted <TM5>
F;238-260/Domain: transmembrane #status predicted <TM6>
F;273-293/Domain: transmembrane #status predicted <TM7>

Query Match 4.1%; Score 13; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 285 LNPLIYSLRNKEV 297
|||||||||||||
Db 285 LNPLIYSLRNKEV 297

RESULT 5
F23701
olfactory receptor I7 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: F23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for odc
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: F23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-327 <BUC>
A;Cross-references: GB:M64386; NID:g205833; PIDN:AAA41749.1; PID:g205834
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 4.1%; Score 13; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAICHPL 130
||||||||||||
Db 123 MAYDRYVAICHPL 135

RESULT 6
A23701
olfactory receptor F3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: A23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for odc
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: A23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-333 <BUC>
A;Cross-references: GB:M64376; NID:g205813; PIDN:AAA41739.1; PID:g205814
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.8%; Score 12; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAICHP 129
||||||||||||
Db 118 MAYDRYVAICHP 129

RESULT 7
D40745
odorant receptor (clone K4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 03-Nov-2000
C;Accession: D40745
R;Ressler, K.J.; Sullivan, S.L.; Buck, L.B.
Cell 73, 597-609, 1993
A;Title: A zonal organization of odorant receptor gene expression in the olfactory epith
A;Reference number: A40745; MUID:93258822; PMID:7683976

A;Accession: D40745
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-222 <RES>
A;Cross-references: GB:L14566; NID:g293753; PIDN:AAA39850.1; PID:g293754
A;Experimental source: olfactory epithelium
A;Note: sequence extracted from NCBI backbone (NCBIP:131753)
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.5%; Score 11; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 YDRYVAICHPL 130
Db 60 YDRYVAICHPL 70

RESULT 8
S29709
olfactory receptor OR14 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C;Accession: S29709
R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer
Nature 361, 353-356, 1993
A;Title: Cloning and expression of odorant receptors.
A;Reference number: S29707; MUID:93149273; PMID:7678922
A;Accession: S29709
A;Molecule type: mRNA
A;Residues: 1-304 <RAM>
C;Superfamily: olfactory receptor OR14

Query Match 3.5%; Score 11; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 285 LNPLIYSLRNK 295
Db 278 LNPLIYSLRNK 288

RESULT 9
S51356
olfactory receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S51356; S47014
R;Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
Eur. J. Biochem. 225, 1157-1168, 1994
A;Title: Olfactory receptor proteins. Expression, characterization and partial purificat
A;Reference number: S51356; MUID:95045546; PMID:7957207
A;Accession: S51356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-309 <GAT>
A;Cross-references: EMBL:X80671; NID:g517365; PIDN:CAA56697.1; PID:g517366
R;Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
submitted to the EMBL Data Library, July 1994
A;Description: Olfactory receptor proteins: expression, characterization and partial pur
A;Reference number: S47014
A;Accession: S47014
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-309 <GA2>
A;Cross-references: EMBL:X80671; NID:g517365; PIDN:CAA56697.1; PID:g517366
C;Superfamily: olfactory receptor OR14

Query Match 3.5%; Score 11; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 285 LNPLIYSLRNK 295
Db 286 LNPLIYSLRNK 296

RESULT 10
I38471
olfactory receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 26-Aug-1999
C;Accession: I38471
R;Ben-Arie, N.; Lancet, D.; Taylor, C.; Khen, M.; Walker, N.; Ledbetter, D.H.; Carrozzo
Hum. Mol. Genet. 3, 229-235, 1994
A;Title: Olfactory receptor gene cluster on human chromosome 17: possible duplication c
A;Reference number: I38470; MUID:94272458; PMID:8004088
A;Accession: I38471
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-165 <RES>
A;Cross-references: EMBL:U04678; NID:g438390; PIDN:AAA18343.1; PID:g438391
C;Genetics:
A;Gene: OR17-4
C;Superfamily: olfactory receptor OR14

Query Match 3.2%; Score 10; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAIC 127
Db 1 MAYDRYVAIC 10

RESULT 11
S28997
G protein-coupled receptor (clone PTE03) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C;Accession: S28997
R;Abe, K.; Kusakabe, Y.; Tanemura, K.; Emori, Y.; Arai, S.
FEBS Lett. 316, 253-256, 1993
A;Title: Multiple genes for G protein-coupled receptors and their expression in lingual
A;Reference number: S28996; MUID:93138133; PMID:8380780
A;Accession: S28997
A;Molecule type: mRNA
A;Residues: 1-168 <ABE>
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.2%; Score 10; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAIC 127
Db 43 MAYDRYVAIC 52

RESULT 12
I38473
olfactory receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 26-Aug-1999
C;Accession: I38473
R;Ben-Arie, N.; Lancet, D.; Taylor, C.; Khen, M.; Walker, N.; Ledbetter, D.H.; Carrozzo,
Hum. Mol. Genet. 3, 229-235, 1994
A;Title: Olfactory receptor gene cluster on human chromosome 17: possible duplication of
A;Reference number: I38470; MUID:94272458; PMID:8004088
A;Accession: I38473
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-215 <RES>
A;Cross-references: EMBL:U04681; NID:g438395; PIDN:AAA18345.1; PID:g438396

C;Genetics:
A;Gene: OR17-30
C;Superfamily: olfactory receptor OR14

Query Match 3.2%; Score 10; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAIC 127
||||||||||
Db 51 MAYDRYVAIC 60

RESULT 13
I38470
olfactory receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 26-Aug-1999
C;Accession: I38470
R;Ben-Arie, N.; Lancet, D.; Taylor, C.; Khen, M.; Walker, N.; Ledbetter, D.H.; Carrozzo,
Hum. Mol. Genet. 3, 229-235, 1994
A;Title: Olfactory receptor gene cluster on human chromosome 17: possible duplication of
A;Reference number: I38470; MUID:94272458; PMID:8004088
A;Accession: I38470
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-216 <RES>
A;Cross-references: EMBL:U04642; NID:g438388; PIDN:AAA17447.1; PID:g438389
C;Genetics:
A;Gene: OR17-2
C;Superfamily: olfactory receptor OR14

Query Match 3.2%; Score 10; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAIC 127
||||||||||
Db 51 MAYDRYVAIC 60

RESULT 14
I38474
olfactory receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 26-Aug-1999
C;Accession: I38474
R;Ben-Arie, N.; Lancet, D.; Taylor, C.; Khen, M.; Walker, N.; Ledbetter, D.H.; Carrozzo,
Hum. Mol. Genet. 3, 229-235, 1994
A;Title: Olfactory receptor gene cluster on human chromosome 17: possible duplication of
A;Reference number: I38470; MUID:94272458; PMID:8004088
A;Accession: I38474
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-216 <RES>
A;Cross-references: EMBL:U04682; NID:g438397; PIDN:AAA18346.1; PID:g438398
C;Genetics:
A;Gene: OR17-32
C;Superfamily: olfactory receptor OR14

Query Match 3.2%; Score 10; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAIC 127
||||||||||
Db 51 MAYDRYVAIC 60

RESULT 15
C40745
odorant receptor (clone K7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C;Accession: C40745
R;Ressler, K.J.; Sullivan, S.L.; Buck, L.B.
Cell 73, 597-609, 1993
A;Title: A zonal organization of odorant receptor gene expression in the olfactory epithe
A;Reference number: A40745; MUID:93258822; PMID:7683976
A;Accession: C40745
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-222 <RES>
A;Cross-references: GB:L14569; NID:g293759; PIDN:AAA39853.1; PID:g293760
A;Experimental source: olfactory epithelium
A;Note: sequence extracted from NCBI backbone (NCBIP:131750)
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.2%; Score 10; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAIC 127
||||||||||
Db 58 MAYDRYVAIC 67

Search completed: October 5, 2004, 14:24:54
Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 5, 2004, 14:09:18 ; Search time 25 Seconds
(without alignments)
658.167 Million cell updates/sec

Title: US-10-024-444B-2
Perfect score: 316
Sequence: 1 MELRNSTLGSGFILVGILND.....VMRALRRVLGKYILLAHSTL 316

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	18.0	316	1	O2AG_HUMAN	Q9h205 homo sapien
2	15	4.7	234	1	GU38_RAT	P35897 rattus norv
3	14	4.4	317	1	OAD1_HUMAN	Q8nge0 homo sapien
4	13	4.1	216	1	O1N1_HUMAN	O43870 homo sapien
5	13	4.1	216	1	O2M4_HUMAN	Q96r27 homo sapien
6	13	4.1	232	1	GU58_RAT	P35899 rattus norv
7	13	4.1	280	1	O1J5_HUMAN	Q9nzp1 homo sapien
8	13	4.1	309	1	O5AK_HUMAN	Q8nh90 homo sapien
9	13	4.1	309	1	O8A1_HUMAN	Q8ngg7 homo sapien
10	13	4.1	310	1	O9Q1_HUMAN	Q8ngq5 homo sapien
11	13	4.1	311	1	O1N3_HUMAN	Q8ngs0 homo sapien
12	13	4.1	311	1	O8H1_HUMAN	Q8ngg4 homo sapien
13	13	4.1	312	1	O2M6_HUMAN	Q8ng83 homo sapien
14	13	4.1	312	1	O2M7_HUMAN	Q8ng81 homo sapien
15	13	4.1	312	1	O8H2_HUMAN	Q8n162 homo sapien
16	13	4.1	312	1	OR17_MOUSE	Q8vgi5 mus musculu
17	13	4.1	313	1	O1J2_HUMAN	Q8ngs2 homo sapien
18	13	4.1	313	1	O1J4_HUMAN	Q8ngs1 homo sapien
19	13	4.1	313	1	OZA4_HUMAN	Q8ngh8 homo sapien
20	13	4.1	314	1	O1C1_HUMAN	Q15619 homo sapien
21	13	4.1	314	1	OR04_MOUSE	Q8vfk1 mus musculu
22	13	4.1	314	1	OR05_MOUSE	Q8vf76 mus musculu
23	13	4.1	314	1	OR11_MOUSE	Q8vgr9 mus musculu
24	13	4.1	314	1	OZA1_HUMAN	Q8ngh5 homo sapien
25	13	4.1	315	1	O2T5_HUMAN	Q8nh02 homo sapien
26	13	4.1	315	1	OZA6_HUMAN	Q8nh54 homo sapien
27	13	4.1	317	1	O6Q1_HUMAN	Q8ngq2 homo sapien
28	13	4.1	319	1	O8K1_HUMAN	Q8ngg5 homo sapien
29	13	4.1	319	1	OAQ1_HUMAN	Q8ngq4 homo sapien
30	13	4.1	319	1	OR10_MOUSE	Q8vgs1 mus musculu
31	13	4.1	320	1	O2T4_HUMAN	Q8nh00 homo sapien
32	13	4.1	320	1	O5C1_HUMAN	Q8ngr4 homo sapien
33	13	4.1	322	1	O1J1_HUMAN	Q8ngs3 homo sapien
34	13	4.1	324	1	O7G2_HUMAN	Q8ng99 homo sapien
35	13	4.1	327	1	OLF7_RAT	P23270 rattus norv
36	13	4.1	331	1	O6B3_HUMAN	Q8ngw1 homo sapien
37	13	4.1	333	1	O7G1_HUMAN	Q8nga0 homo sapien
38	13	4.1	337	1	O1FC_HUMAN	Q8nha8 homo sapien
39	12	3.8	298	1	O5K3_HUMAN	Q8nh89 homo sapien
40	12	3.8	309	1	OAV1_HUMAN	Q8ngi7 homo sapien
41	12	3.8	311	1	O5AN_HUMAN	Q8ngi8 homo sapien
42	12	3.8	311	1	O5P3_HUMAN	Q8wz94 homo sapien
43	12	3.8	314	1	OR23_MOUSE	Q8vg09 mus musculu
44	12	3.8	315	1	O5A1_HUMAN	Q8ngj0 homo sapien
45	12	3.8	322	1	O5P2_HUMAN	Q8wz92 homo sapien

ALIGNMENTS

```
RESULT 1
O2AG_HUMAN
ID   O2AG_HUMAN     STANDARD;      PRT;   316 AA.
AC   Q9H205; Q96R26;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 2AG1 (HT3).
GN   OR2AG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 68-284 FROM N.A.
RX   MEDLINE=22202146; PubMed=12213199;
RA   Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA   Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA   Lehrach H., Lancet D., Shamir R.;
RT   "DEFOG: a practical scheme for deciphering families of genes.";
RL   Genomics 80:295-302(2002).
RN   [3]
RP   SEQUENCE OF 152-316 FROM N.A.
RX   MEDLINE=21310002; PubMed=11416212;
RA   Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
RA   Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT   "Genomic analysis of orthologous mouse and human olfactory receptor
RT   loci.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB065823; BAC06042.1; -.
DR   EMBL; AF399618; AAK95103.1; -.
DR   EMBL; AF321237; AAG45209.1; -.
DR   Genew; HGNC:15142; OR2AG1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
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DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN       1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26    49       1 (POTENTIAL).
FT   DOMAIN       50    57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58    79       2 (POTENTIAL).
FT   DOMAIN       80    100      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     101   120      3 (POTENTIAL).
FT   DOMAIN       121   139      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     140   158      4 (POTENTIAL).
FT   DOMAIN       159   195      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     196   219      5 (POTENTIAL).
FT   DOMAIN       220   236      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     237   259      6 (POTENTIAL).
FT   DOMAIN       260   272      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     273   292      7 (POTENTIAL).
FT   DOMAIN       293   316      CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189      BY SIMILARITY.
FT   CARBOHYD     5     5        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     19    19       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     187   187      V -> L (IN REF. 3).
FT   CONFLICT     299   299      R -> G (IN REF. 3).
SQ   SEQUENCE   316 AA;  35270 MW;  6885161BD606C0AE CRC64;

  Query Match             18.0%;  Score 57;  DB 1;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-48;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 EARLHMPMYLLLGQLSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMG 108


RESULT 2
GU38_RAT
ID   GU38_RAT       STANDARD;      PRT;   234 AA.
AC   P35897;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Possible gustatory receptor clone PTE38 (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Fischer; TISSUE=Lingual epithelium;
RX   MEDLINE=93138133; PubMed=8380780;
RA   Abe K., Kusakabe Y., Tanemura K., Emori Y., Arai S.;
RT   "Multiple genes for G protein-coupled receptors and their expression
RT   in lingual epithelia.";
RL   FEBS Lett. 316:253-256(1993).
CC   -!- FUNCTION: Possible taste receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Tongue specific.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   NON_TER      1     1
FT   TRANSMEM     <1    11       2 (POTENTIAL).
FT   DOMAIN       12    42       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     43    62       3 (POTENTIAL).
FT   DOMAIN       63    84       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     85    105      4 (POTENTIAL).
FT   DOMAIN       106   138      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     139   160      5 (POTENTIAL).
FT   DOMAIN       161   182      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     183   202      6 (POTENTIAL).
FT   DOMAIN       203   212      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     213   234      7 (POTENTIAL).
FT   DISULFID     39    121      BY SIMILARITY.
FT   NON_TER      234   234
SQ   SEQUENCE   234 AA;  26375 MW;  B4506DD948080003 CRC64;

  Query Match             4.7%;  Score 15;  DB 1;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPLKY 132
              |||||||||||||||
Db         60 MAYDRYVAICHPLKY 74


RESULT 3
OAD1_HUMAN
ID   OAD1_HUMAN     STANDARD;      PRT;   317 AA.
AC   Q8NGE0;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 10AD1.
GN   OR10AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB065872; BAC06090.1; -.
DR   Genew; HGNC:14819; OR10AD1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN       1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26    46       1 (POTENTIAL).
FT   DOMAIN       47    55       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     56    76       2 (POTENTIAL).
FT   DOMAIN       77    100      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     101   121      3 (POTENTIAL).
FT   DOMAIN       122   140      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     141   161      4 (POTENTIAL).
FT   DOMAIN       162   198      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     199   218      5 (POTENTIAL).
FT   DOMAIN       219   238      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     239   259      6 (POTENTIAL).
FT   DOMAIN       260   272      EXTRACELLULAR (POTENTIAL).
```

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FT   TRANSMEM     273    293       7 (POTENTIAL).
FT   DOMAIN       294    317       CYTOPLASMIC (POTENTIAL).
FT   DISULFID      98    190       BY SIMILARITY.
FT   CARBOHYD       4      4       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   317 AA;  35698 MW;  72D856594467060F CRC64;

  Query Match             4.4%;  Score 14;  DB 1;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        114 LLAFMAYDRYVAIC 127
              ||||||||||||||
Db        115 LLAFMAYDRYVAIC 128


RESULT 4
O1N1_HUMAN
ID   O1N1_HUMAN     STANDARD;      PRT;   216 AA.
AC   O43870;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 1N1 (Olfactory receptor 1-26) (OR1-26) (Fragment).
GN   OR1N1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98160182; PubMed=9500546;
RA   Rouquier S., Taviaux S., Trask B.J., Brand-Arpon V., van den Engh G.,
RA   Demaille J.G., Giorgi D.;
RT   "Distribution of olfactory receptor genes in the human genome.";
RL   Nat. Genet. 18:243-250(1998).
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U86216; AAC39612.1; -.
DR   Genew; HGNC:8221; OR1N1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Multigene family;
KW   Olfaction.
FT   NON_TER       1      1
FT   TRANSMEM     <1     12       2 (POTENTIAL).
FT   DOMAIN       13     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     53       3 (POTENTIAL).
FT   DOMAIN       54     72       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     73     91       4 (POTENTIAL).
FT   DOMAIN       92    129       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    130    152       5 (POTENTIAL).
FT   DOMAIN      153    169       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    170    192       6 (POTENTIAL).
FT   DOMAIN      193    205       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    206   >216       7 (POTENTIAL).
FT   DISULFID     30    122       BY SIMILARITY.
FT   NON_TER     216    216
SQ   SEQUENCE   216 AA;  23896 MW;  E27DA9AE1E2C50BE CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 216;
  Best Local Similarity   100.0%;  Pred. No. 4e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db         51 MAYDRYVAICHPL 63


RESULT 5
O2M4_HUMAN
ID   O2M4_HUMAN     STANDARD;      PRT;   216 AA.
AC   Q96R27; Q15611;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 2M4 (Olfactory receptor TPCR100) (OST710)
DE   (HTPCRX18) (Fragment).
GN   OR2M4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22202146; PubMed=12213199;
RA   Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA   Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA   Lehrach H., Lancet D., Shamir R.;
RT   "DEFOG: a practical scheme for deciphering families of genes.";
RL   Genomics 80:295-302(2002).
RN   [2]
RP   SEQUENCE OF 59-215 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=97224452; PubMed=9119360;
RA   Vanderhaeghen P., Schurmans S., Vassart G., Parmentier M.;
RT   "Specific repertoire of olfactory receptor genes in the male germ
RT   cells of several mammalian species.";
RL   Genomics 39:239-246(1997).
RN   [3]
RP   SEQUENCE OF 59-172 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=92131132; PubMed=1370859;
RA   Parmentier M., Libert F., Schurmans S., Schiffmann S., Lefort A.,
RA   Eggerickx D., Ledent C., Mollereau C., Gerard C., Perret J.,
RA   Grootegoed A., Vassart G.;
RT   "Expression of members of the putative olfactory receptor gene family
RT   in mammalian germ cells.";
RL   Nature 355:453-455(1992).
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF399617; AAK95102.1; -.
DR   EMBL; X89666; CAA61813.1; -.
DR   EMBL; X64992; -; NOT_ANNOTATED_CDS.
DR   PIR; S58011; S58011.
DR   Genew; HGNC:8270; OR2M4.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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KW   G-protein coupled receptor; Transmembrane; Multigene family;
KW   Olfaction.
FT   NON_TER       1      1
FT   TRANSMEM     <1     12       2 (POTENTIAL).
FT   DOMAIN       13     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     53       3 (POTENTIAL).
FT   DOMAIN       54     72       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     73     91       4 (POTENTIAL).
FT   DOMAIN       92    128       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    129    152       5 (POTENTIAL).
FT   DOMAIN      153    169       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    170    192       6 (POTENTIAL).
FT   DOMAIN      193    205       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    206   >216       7 (POTENTIAL).
FT   DISULFID     30    122       BY SIMILARITY.
FT   CONFLICT    214    215       LT -> SH (IN REF. 2).
FT   NON_TER     216    216
SQ   SEQUENCE   216 AA;  23872 MW;  DE7432325A5AACF9 CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 216;
  Best Local Similarity   100.0%;  Pred. No. 4e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db         51 MAYDRYVAICHPL 63


RESULT 6
GU58_RAT
ID   GU58_RAT       STANDARD;      PRT;   232 AA.
AC   P35899;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Possible gustatory receptor clone PTE58 (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Fischer; TISSUE=Lingual epithelium;
RX   MEDLINE=93138133; PubMed=8380780;
RA   Abe K., Kusakabe Y., Tanemura K., Emori Y., Arai S.;
RT   "Multiple genes for G protein-coupled receptors and their expression
RT   in lingual epithelia.";
RL   FEBS Lett. 316:253-256(1993).
CC   -!- FUNCTION: Possible taste receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Tongue specific.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   PIR; S29001; S29001.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   NON_TER       1      1
FT   TRANSMEM     <1      9       2 (POTENTIAL).
FT   DOMAIN       10     40       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     41     60       3 (POTENTIAL).
FT   DOMAIN       61     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     83    103       4 (POTENTIAL).
FT   DOMAIN      104    136       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    137    158       5 (POTENTIAL).
FT   DOMAIN      159    180       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    181    200       6 (POTENTIAL).
FT   DOMAIN      201    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    232       7 (POTENTIAL).
FT   DISULFID     37    119       BY SIMILARITY.
FT   NON_TER     232    232
SQ   SEQUENCE   232 AA;  25695 MW;  2B72EEAB08A992B7 CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db         58 MAYDRYVAICHPL 70


RESULT 7
O1J5_HUMAN
ID   O1J5_HUMAN     STANDARD;      PRT;   280 AA.
AC   Q9NZP1;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 1J5 (HSA5) (HTPCRX15) (Fragment).
GN   OR1J5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 91-252 FROM N.A.
RX   MEDLINE=20183981; PubMed=10706615;
RA   Rouquier S., Blancher A., Giorgi D.;
RT   "The olfactory receptor gene repertoire in primates and mouse:
RT   Evidence for reduction of the functional fraction in primates.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
RN   [2]
RP   SEQUENCE OF 93-206 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=92131132; PubMed=1370859;
RA   Parmentier M., Libert F., Schurmans S., Schiffmann S., Lefort A.,
RA   Eggerickx D., Ledent C., Mollereau C., Gerard C., Perret J.,
RA   Grootegoed A., Vassart G.;
RT   "Expression of members of the putative olfactory receptor gene family
RT   in mammalian germ cells.";
RL   Nature 355:453-455(1992).
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF179767; AAF40352.1; -.
DR   EMBL; X64989; -; NOT_ANNOTATED_CDS.
DR   Genew; HGNC:15109; OR1J5.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Multigene family;
KW   Olfaction.
FT   NON_TER       1      1
FT   TRANSMEM     <1     16       1 (POTENTIAL).
FT   DOMAIN       17     24       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     25     46       2 (POTENTIAL).
FT   DOMAIN       47     67       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     68     87       3 (POTENTIAL).
FT   DOMAIN       88    106       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    107    125       4 (POTENTIAL).
FT   DOMAIN      126    163       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    164    186       5 (POTENTIAL).
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FT   DOMAIN       187    203       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     204    226       6 (POTENTIAL).
FT   DOMAIN       227    239       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     240    259       7 (POTENTIAL).
FT   DOMAIN       260    280       CYTOPLASMIC (POTENTIAL).
FT   DISULFID      64    156       BY SIMILARITY.
FT   CONFLICT     115    115       S -> T (IN REF. 1).
SQ   SEQUENCE   280 AA;  31788 MW;  3ACC2B01C948791D CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 5e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db         85 MAYDRYVAICHPL 97


RESULT 8
O5AK_HUMAN
ID   O5AK_HUMAN      STANDARD;      PRT;   309 AA.
AC   Q8NH90;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 5AK2.
GN   OR5AK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB065496; BAC05747.1; -.
DR   Genew; HGNC:15251; OR5AK2.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN         1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      26     46       1 (POTENTIAL).
FT   DOMAIN        47     54       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      55     75       2 (POTENTIAL).
FT   DOMAIN        76     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     100    120       3 (POTENTIAL).
FT   DOMAIN       121    133       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     134    154       4 (POTENTIAL).
FT   DOMAIN       155    196       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     197    217       5 (POTENTIAL).
FT   DOMAIN       218    237       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     238    258       6 (POTENTIAL).
FT   DOMAIN       259    271       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     272    292       7 (POTENTIAL).
FT   DOMAIN       293    309       CYTOPLASMIC (POTENTIAL).
FT   DISULFID      97    189       BY SIMILARITY.
FT   CARBOHYD       5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     155    155       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     265    265       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   309 AA;  34627 MW;  6022418115A44AC4 CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        285 LNPLIYSLRNKEV 297
              |||||||||||||
Db        285 LNPLIYSLRNKEV 297


RESULT 9
O8A1_HUMAN
ID   O8A1_HUMAN      STANDARD;      PRT;   309 AA.
AC   Q8NGG7; Q96RC6;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 8A1 (OST025).
GN   OR8A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 68-282 FROM N.A.
RX   MEDLINE=22202146; PubMed=12213199;
RA   Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA   Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA   Lehrach H., Lancet D., Shamir R.;
RT   "DEFOG: a practical scheme for deciphering families of genes.";
RL   Genomics 80:295-302(2002).
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB065833; BAC06052.1; -.
DR   EMBL; AF399512; AAK94997.1; -.
DR   Genew; HGNC:8469; OR8A1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN         1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      26     46       1 (POTENTIAL).
FT   DOMAIN        47     54       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      55     75       2 (POTENTIAL).
```

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FT   DOMAIN       76     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    100    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    160       4 (POTENTIAL).
FT   DOMAIN      161    196       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    197    216       5 (POTENTIAL).
FT   DOMAIN      217    236       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    237    257       6 (POTENTIAL).
FT   DOMAIN      258    270       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    271    291       7 (POTENTIAL).
FT   DOMAIN      292    309       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    188       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   309 AA;  34395 MW;  202DEE98B0F4EEED CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db        118 MAYDRYVAICHPL 130


RESULT 10
O9Q1_HUMAN
ID   O9Q1_HUMAN     STANDARD;      PRT;   310 AA.
AC   Q8NGQ5; Q96RA7;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 9Q1.
GN   OR9Q1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 68-282 FROM N.A.
RX   MEDLINE=22202146; PubMed=12213199;
RA   Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA   Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA   Lehrach H., Lancet D., Shamir R.;
RT   "DEFOG: a practical scheme for deciphering families of genes.";
RL   Genomics 80:295-302(2002).
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB065734; BAC05955.1; -.
DR   EMBL; AF399532; AAK95017.1; -.
DR   Genew; HGNC:14724; OR9Q1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN       1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    26     46       1 (POTENTIAL).
FT   DOMAIN      47     54       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    55     75       2 (POTENTIAL).
FT   DOMAIN      76     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   100    120       3 (POTENTIAL).
FT   DOMAIN     121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   140    160       4 (POTENTIAL).
FT   DOMAIN     161    197       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   198    217       5 (POTENTIAL).
FT   DOMAIN     218    236       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   237    257       6 (POTENTIAL).
FT   DOMAIN     258    270       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   271    291       7 (POTENTIAL).
FT   DOMAIN     292    310       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    97    189       BY SIMILARITY.
FT   CARBOHYD     5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   310 AA;  34756 MW;  6C27C347AE8FD741 CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        285 LNPLIYSLRNKEV 297
              |||||||||||||
Db        284 LNPLIYSLRNKEV 296


RESULT 11
O1N3_HUMAN
ID   O1N3_HUMAN     STANDARD;      PRT;   311 AA.
AC   Q8NGS0; Q96R93;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 1N3.
GN   OR1N3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 66-281 FROM N.A.
RX   MEDLINE=22202146; PubMed=12213199;
RA   Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA   Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA   Lehrach H., Lancet D., Shamir R.;
RT   "DEFOG: a practical scheme for deciphering families of genes.";
RL   Genomics 80:295-302(2002).
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
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DR   EMBL; AB065719; BAC05940.1; -.
DR   EMBL; AF399547; AAK95032.1; -.
DR   Genew; HGNC:15112; OR1N3.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     23       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     24     47       1 (POTENTIAL).
FT   DOMAIN       48     55       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     56     77       2 (POTENTIAL).
FT   DOMAIN       78     98       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     99    118       3 (POTENTIAL).
FT   DOMAIN      119    137       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    138    156       4 (POTENTIAL).
FT   DOMAIN      157    194       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    195    217       5 (POTENTIAL).
FT   DOMAIN      218    234       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    235    257       6 (POTENTIAL).
FT   DOMAIN      258    270       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    271    290       7 (POTENTIAL).
FT   DOMAIN      291    311       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     95    187       BY SIMILARITY.
FT   CARBOHYD      3      3       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   311 AA;  34650 MW;  6B82AE0B4A836180 CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 311;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db        116 MAYDRYVAICHPL 128


RESULT 12
O8H1_HUMAN
ID   O8H1_HUMAN     STANDARD;      PRT;   311 AA.
AC   Q8NGG4;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 8H1.
GN   OR8H1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB065836; BAC06055.1; -.
DR   Genew; HGNC:14824; OR8H1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     46       1 (POTENTIAL).
FT   DOMAIN       47     54       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     55     75       2 (POTENTIAL).
FT   DOMAIN       76     98       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     99    119       3 (POTENTIAL).
FT   DOMAIN      120    138       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    139    159       4 (POTENTIAL).
FT   DOMAIN      160    196       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    197    216       5 (POTENTIAL).
FT   DOMAIN      217    236       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    237    257       6 (POTENTIAL).
FT   DOMAIN      258    270       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    271    291       7 (POTENTIAL).
FT   DOMAIN      292    311       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     96    188       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   311 AA;  35227 MW;  B2E5484AE80C2BB2 CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 311;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        285 LNPLIYSLRNKEV 297
              |||||||||||||
Db        284 LNPLIYSLRNKEV 296


RESULT 13
O2M6_HUMAN
ID   O2M6_HUMAN     STANDARD;      PRT;   312 AA.
AC   Q8NG83;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 2M6.
GN   OR2M6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB065952; BAC06165.1; -.
DR   Genew; HGNC:19593; OR2M6.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
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DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     49       1 (POTENTIAL).
FT   DOMAIN       50     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     79       2 (POTENTIAL).
FT   DOMAIN       80    100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    101    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    158       4 (POTENTIAL).
FT   DOMAIN      159    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    219       5 (POTENTIAL).
FT   DOMAIN      220    236       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    237    259       6 (POTENTIAL).
FT   DOMAIN      260    272       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    273    292       7 (POTENTIAL).
FT   DOMAIN      293    311       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   312 AA;  34827 MW;  5CEF428A1948C2F2 CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        285 LNPLIYSLRNKEV 297
              |||||||||||||
Db        285 LNPLIYSLRNKEV 297


RESULT 14
O2M7_HUMAN
ID   O2M7_HUMAN     STANDARD;      PRT;   312 AA.
AC   Q8NG81;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 2M7.
GN   OR2M7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB065954; BAC06167.1; -.
DR   Genew; HGNC:19594; OR2M7.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     49       1 (POTENTIAL).
FT   DOMAIN       50     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     79       2 (POTENTIAL).
FT   DOMAIN       80    100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    101    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    158       4 (POTENTIAL).
FT   DOMAIN      159    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    219       5 (POTENTIAL).
FT   DOMAIN      220    236       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    237    259       6 (POTENTIAL).
FT   DOMAIN      260    272       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    273    292       7 (POTENTIAL).
FT   DOMAIN      293    311       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   312 AA;  34902 MW;  42A9A1D7EB861E88 CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        285 LNPLIYSLRNKEV 297
              |||||||||||||
Db        285 LNPLIYSLRNKEV 297


RESULT 15
O8H2_HUMAN
ID   O8H2_HUMAN     STANDARD;      PRT;   312 AA.
AC   Q8N162;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Olfactory receptor 8H2.
GN   OR8H2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Putative odorant receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC       WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB065657; BAC05883.1; -.
DR   EMBL; AB065845; BAC06063.1; -.
DR   Genew; HGNC:15308; OR8H2.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
```

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KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     26       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     27     47       1 (POTENTIAL).
FT   DOMAIN       48     55       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     56     76       2 (POTENTIAL).
FT   DOMAIN       77     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    100    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    160       4 (POTENTIAL).
FT   DOMAIN      161    197       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    198    217       5 (POTENTIAL).
FT   DOMAIN      218    237       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    238    258       6 (POTENTIAL).
FT   DOMAIN      259    271       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    272    292       7 (POTENTIAL).
FT   DOMAIN      293    312       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189       BY SIMILARITY.
FT   CARBOHYD      6      6       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   312 AA;  35422 MW;  0D5112EF980EC13E CRC64;

  Query Match             4.1%;  Score 13;  DB 1;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        285 LNPLIYSLRNKEV 297
              |||||||||||||
Db        285 LNPLIYSLRNKEV 297


Search completed: October  5, 2004, 14:22:10
Job time : 31 secs
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OM protein - protein search, using sw model

Run on: October 5, 2004, 14:17:19 ; Search time 117 Seconds
(without alignments)
852.169 Million cell updates/sec

Title: US-10-024-444B-2
Perfect score: 316
Sequence: 1 MELRNSTLGSGFILVGILND.....VMRALRRVLGKYILLAHSTL 316

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	13.6	316	11	Q9D4F9	Q9d4f9 mus musculu
2	43	13.6	316	11	Q9D3U9	Q9d3u9 mus musculu
3	29	9.2	316	11	Q9EPF8	Q9epf8 mus musculu
4	28	8.9	316	11	Q8VGU0	Q8vgu0 mus musculu
5	28	8.9	316	11	Q9EPF7	Q9epf7 mus musculu
6	28	8.9	316	11	Q7TRN2	Q7trn2 mus musculu
7	23	7.3	311	11	Q8VFM6	Q8vfm6 mus musculu
8	23	7.3	311	11	Q7TRN4	Q7trn4 mus musculu
9	23	7.3	315	11	Q8VF88	Q8vf88 mus musculu
10	23	7.3	316	11	Q8VF89	Q8vf89 mus musculu
11	23	7.3	316	11	Q8VFM5	Q8vfm5 mus musculu
12	23	7.3	319	11	Q9EPF5	Q9epf5 mus musculu
13	21	6.6	316	11	Q7TRN3	Q7trn3 mus musculu
14	21	6.6	317	11	Q8VFM4	Q8vfm4 mus musculu
15	18	5.7	315	11	Q8VFM3	Q8vfm3 mus musculu
16	17	5.4	312	11	Q7TS14	Q7ts14 mus musculu
17	17	5.4	315	11	Q9EPF6	Q9epf6 mus musculu
18	17	5.4	317	11	Q7TS16	Q7ts16 mus musculu
19	17	5.4	317	11	Q7TS15	Q7ts15 mus musculu
20	15	4.7	312	11	Q8VFF6	Q8vff6 mus musculu
21	15	4.7	313	11	Q7TS23	Q7ts23 mus musculu
22	15	4.7	313	11	Q7TRD5	Q7trd5 mus musculu
23	15	4.7	316	11	Q8VGD1	Q8vgd1 mus musculu
24	15	4.7	327	11	Q8VF22	Q8vf22 mus musculu
25	14	4.4	317	4	Q8NGE0	Q8nge0 homo sapien
26	13	4.1	172	4	Q8WZ85	Q8wz85 homo sapien
27	13	4.1	175	11	O55018	O55018 mus musculu
28	13	4.1	175	11	O55019	O55019 mus musculu
29	13	4.1	175	11	Q925E9	Q925e9 mus musculu
30	13	4.1	215	11	Q9EPZ1	Q9epz1 mus musculu
31	13	4.1	216	6	Q9N207	Q9n207 callithrix
32	13	4.1	216	6	Q9N1Z1	Q9n1z1 saimiri sci
33	13	4.1	216	6	Q9N202	Q9n202 callithrix
34	13	4.1	216	6	Q9GKF6	Q9gkf6 ornithorhyn
35	13	4.1	216	6	Q9N1Z3	Q9n1z3 saimiri bol
36	13	4.1	216	6	Q9N209	Q9n209 macaca sylv
37	13	4.1	216	6	Q9GKI0	Q9gki0 phascolarct
38	13	4.1	216	6	Q9GKG1	Q9gkg1 ornithorhyn
39	13	4.1	216	6	Q9GKF2	Q9gkf2 ornithorhyn
40	13	4.1	216	6	Q9N213	Q9n213 macaca sylv
41	13	4.1	216	6	Q9N220	Q9n220 eulemur ful
42	13	4.1	216	6	Q9N205	Q9n205 callithrix
43	13	4.1	216	6	Q9N1Y6	Q9n1y6 saimiri sci
44	13	4.1	216	11	Q9JM32	Q9jm32 mus musculu
45	13	4.1	216	11	Q9JM18	Q9jm18 mus musculu

ALIGNMENTS

RESULT 1
Q9D4F9
ID Q9D4F9 PRELIMINARY; PRT; 316 AA.
AC Q9D4F9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 4932441H21Rik protein.
GN 4933433E02RIK OR 4932441H21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK016560; BAB30304.1; -.
DR MGD; MGI:1914036; 4933433E02Rik.

```
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ   SEQUENCE   316 AA;  34930 MW;  231E89FABCB207BA CRC64;

  Query Match             13.6%;  Score 43;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-36;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        255 ATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEV 297
              |||||||||||||||||||||||||||||||||||||||||||||
Db        255 ATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEV 297


RESULT 2
Q9D3U9
ID   Q9D3U9      PRELIMINARY;      PRT;   316 AA.
AC   Q9D3U9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   4933433E02Rik protein (Olfactory receptor MOR283-1) (Olfactory
DE   receptor GA_x6K02T2PBJ9-9195805-9196755).
GN   4933433E02RIK OR GA_X6K02T2PBJ9-9195805-9196755.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK017036; BAB30564.1; -.
DR   EMBL; AY073025; AAL60688.1; -.
DR   EMBL; AY317822; AAP71166.1; -.
DR   MGD; MGI:1914036; 4933433E02Rik.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   316 AA;  34916 MW;  C2C5338B675D3225 CRC64;

  Query Match             13.6%;  Score 43;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-36;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        255 ATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEV 297
              |||||||||||||||||||||||||||||||||||||||||||||
Db        255 ATFMYVLPSSFHSPKQDNIISVFYTIVTPALNPLIYSLRNKEV 297


RESULT 3
Q9EPF8
ID   Q9EPF8      PRELIMINARY;      PRT;   316 AA.
AC   Q9EPF8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T1 olfactory receptor (Olfactory receptor MOR283-11) (Olfactory
DE   receptor GA_x6K02T2PBJ9-9271198-9270248).
GN   GA_X6K02T2PBJ9-9271198-9270248.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=21310002; PubMed=11416212;
RA   Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
RA   Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT   "Genomic analysis of orthologous mouse and human olfactory receptor
RT   loci.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF321234; AAG45195.1; -.
DR   EMBL; AY073740; AAL61403.1; -.
DR   EMBL; AY317827; AAP71171.1; -.
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DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   316 AA;  34981 MW;  5D89BF1BEB17D480 CRC64;

  Query Match             9.2%;  Score 29;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-21;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        269 KQDNIISVFYTIVTPALNPLIYSLRNKEV 297
              |||||||||||||||||||||||||||||
Db        269 KQDNIISVFYTIVTPALNPLIYSLRNKEV 297


RESULT 4
Q8VGU0
ID   Q8VGU0      PRELIMINARY;      PRT;   316 AA.
AC   Q8VGU0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Olfactory receptor MOR283-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073056; AAL60719.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   316 AA;  35239 MW;  2E05EB66442A34C6 CRC64;

  Query Match             8.9%;  Score 28;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        270 QDNIISVFYTIVTPALNPLIYSLRNKEV 297
              |||||||||||||||||||||||||||||
Db        270 QDNIISVFYTIVTPALNPLIYSLRNKEV 297


RESULT 5
Q9EPF7
ID   Q9EPF7      PRELIMINARY;      PRT;   316 AA.
AC   Q9EPF7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   T2 olfactory receptor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=21310002; PubMed=11416212;
RA   Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
RA   Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT   "Genomic analysis of orthologous mouse and human olfactory receptor
RT   loci.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
DR   EMBL; AF321234; AAG45196.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   316 AA;  35252 MW;  B50299F55D161A1E CRC64;

  Query Match             8.9%;  Score 28;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        270 QDNIISVFYTIVTPALNPLIYSLRNKEV 297
              |||||||||||||||||||||||||||||
Db        270 QDNIISVFYTIVTPALNPLIYSLRNKEV 297


RESULT 6
Q7TRN2
ID   Q7TRN2      PRELIMINARY;      PRT;   316 AA.
AC   Q7TRN2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Olfactory receptor GA_x6K02T2PBJ9-9256348-9255398.
GN   GA_X6K02T2PBJ9-9256348-9255398.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY317826; AAP71170.1; -.
KW   Receptor.
SQ   SEQUENCE   316 AA;  35266 MW;  6318EB66443EB21D CRC64;

  Query Match             8.9%;  Score 28;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-20;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        270 QDNIISVFYTIVTPALNPLIYSLRNKEV 297
              |||||||||||||||||||||||||||||
Db        270 QDNIISVFYTIVTPALNPLIYSLRNKEV 297


RESULT 7
Q8VFM6
ID   Q8VFM6      PRELIMINARY;      PRT;   311 AA.
AC   Q8VFM6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
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DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Olfactory receptor MOR283-3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073495; AAL61158.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   311 AA;  34194 MW;  90113F7C8BF8D20C CRC64;

  Query Match             7.3%;  Score 23;  DB 11;  Length 311;
  Best Local Similarity   100.0%;  Pred. No. 4e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        275 SVFYTIVTPALNPLIYSLRNKEV 297
              |||||||||||||||||||||||
Db        275 SVFYTIVTPALNPLIYSLRNKEV 297


RESULT 8
Q7TRN4
ID   Q7TRN4      PRELIMINARY;      PRT;   311 AA.
AC   Q7TRN4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Olfactory receptor GA_x6K02T2PBJ9-9130754-9129519.
GN   GA_X6K02T2PBJ9-9130754-9129519.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY317819; AAP71163.1; -.
KW   Receptor.
SQ   SEQUENCE   311 AA;  34182 MW;  1338254FA2F8D21D CRC64;

  Query Match             7.3%;  Score 23;  DB 11;  Length 311;
  Best Local Similarity   100.0%;  Pred. No. 4e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        275 SVFYTIVTPALNPLIYSLRNKEV 297
              |||||||||||||||||||||||
Db        275 SVFYTIVTPALNPLIYSLRNKEV 297


RESULT 9
Q8VF88
ID   Q8VF88      PRELIMINARY;      PRT;   315 AA.
AC   Q8VF88;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Olfactory receptor MOR283-9 (Olfactory receptor
DE   GA_x6K02T2PBJ9-9067220-9066273).
GN   GA_X6K02T2PBJ9-9067220-9066273.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073646; AAL61309.1; -.
DR   EMBL; AY317815; AAP71160.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   315 AA;  34927 MW;  9A9E426357BA710C CRC64;

  Query Match             7.3%;  Score 23;  DB 11;  Length 315;
  Best Local Similarity   100.0%;  Pred. No. 4e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        108 GSAEDLLLAFMAYDRYVAICHPL 130
              |||||||||||||||||||||||
Db        108 GSAEDLLLAFMAYDRYVAICHPL 130


RESULT 10
Q8VF89
ID   Q8VF89      PRELIMINARY;      PRT;   316 AA.
AC   Q8VF89;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Olfactory receptor MOR283-8 (Olfactory receptor
DE   GA_x6K02T2PBJ9-9055944-9054994).
GN   GA_X6K02T2PBJ9-9055944-9054994.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
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RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073645; AAL61308.1; -.
DR   EMBL; AY317814; AAP71159.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   316 AA;  35153 MW;  2123AF7831AFA228 CRC64;

  Query Match             7.3%;  Score 23;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 4e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        108 GSAEDLLLAFMAYDRYVAICHPL 130
              |||||||||||||||||||||||
Db        108 GSAEDLLLAFMAYDRYVAICHPL 130


RESULT 11
Q8VFM5
ID   Q8VFM5      PRELIMINARY;      PRT;   316 AA.
AC   Q8VFM5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Olfactory receptor MOR283-4 (Olfactory receptor
DE   GA_x6K02T2PBJ9-9184187-9183237).
GN   GA_X6K02T2PBJ9-9184187-9183237.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073497; AAL61160.1; -.
DR   EMBL; AY317821; AAP71165.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   316 AA;  35283 MW;  3D944A8FAA1A7436 CRC64;

  Query Match             7.3%;  Score 23;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 4e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        275 SVFYTIVTPALNPLIYSLRNKEV 297
              |||||||||||||||||||||||
Db        275 SVFYTIVTPALNPLIYSLRNKEV 297


RESULT 12
Q9EPF5
ID   Q9EPF5      PRELIMINARY;      PRT;   319 AA.
AC   Q9EPF5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   T4 olfactory receptor (Olfactory receptor MOR283-7) (Olfactory
DE   receptor GA_x6K02T2PBJ9-9222217-9223176).
GN   GA_X6K02T2PBJ9-9222217-9223176.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=21310002; PubMed=11416212;
RA   Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
RA   Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT   "Genomic analysis of orthologous mouse and human olfactory receptor
RT   loci.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF321234; AAG45198.1; -.
DR   EMBL; AY073501; AAL61164.1; -.
DR   EMBL; AY317824; AAP71168.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
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DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   319 AA;  35493 MW;  8CFB7EC7A5DBD3D8 CRC64;

  Query Match             7.3%;  Score 23;  DB 11;  Length 319;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        108 GSAEDLLLAFMAYDRYVAICHPL 130
              |||||||||||||||||||||||
Db        108 GSAEDLLLAFMAYDRYVAICHPL 130


RESULT 13
Q7TRN3
ID   Q7TRN3      PRELIMINARY;      PRT;   316 AA.
AC   Q7TRN3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Olfactory receptor GA_x6K02T2PBJ9-9168355-9167405.
GN   GA_X6K02T2PBJ9-9168355-9167405.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY317820; AAP71164.1; -.
KW   Receptor.
SQ   SEQUENCE   316 AA;  35091 MW;  3CFBC85EC2B005D3 CRC64;

  Query Match             6.6%;  Score 21;  DB 11;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 5e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        110 AEDLLLAFMAYDRYVAICHPL 130
              |||||||||||||||||||||
Db        110 AEDLLLAFMAYDRYVAICHPL 130


RESULT 14
Q8VFM4
ID   Q8VFM4      PRELIMINARY;      PRT;   317 AA.
AC   Q8VFM4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Olfactory receptor MOR283-5 (Olfactory receptor
DE   GA_x6K02T2PBJ9-9119301-9118348).
GN   GA_X6K02T2PBJ9-9119301-9118348.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073498; AAL61161.1; -.
DR   EMBL; AY317818; AAP71162.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   317 AA;  35471 MW;  C5F1B706E5437F73 CRC64;

  Query Match             6.6%;  Score 21;  DB 11;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 5e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        110 AEDLLLAFMAYDRYVAICHPL 130
              |||||||||||||||||||||
Db        110 AEDLLLAFMAYDRYVAICHPL 130


RESULT 15
Q8VFM3
ID   Q8VFM3      PRELIMINARY;      PRT;   315 AA.
AC   Q8VFM3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Olfactory receptor MOR283-6 (Olfactory receptor
DE   GA_x6K02T2PBJ9-9092181-9091234).
GN   GA_X6K02T2PBJ9-9092181-9091234.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA   Walker M., Williams E.M., Axel R., Trask B.J.;
RT   "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT   genes, extensive alternate splicing, and unequal expression levels.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Sanders K.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073499; AAL61162.1; -.
DR   EMBL; AY317816; AAP71161.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
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DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 315 AA; 35179 MW; AC02001D733D1736 CRC64;

Query Match 5.7%; Score 18; DB 11; Length 315;
Best Local Similarity 100.0%; Pred. No. 6.8e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NSTLGSGFILVGILNDSG 22
||||||||||||||||||
Db 5 *NSTLGSGFILVGILNDSG* 22

Search completed: October 5, 2004, 14:24:09
Job time : 120 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 5, 2004, 14:21:12 ; Search time 41 Seconds
(without alignments)
397.898 Million cell updates/sec

Title: US-10-024-444B-2
Perfect score: 316
Sequence: 1 MELRNSTLGSGFILVGILND.....VMRALRRVLGKYILLAHSTL 316

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	4.1	222	4	US-09-465-901-44	Sequence 44, Appl
2	13	4.1	223	4	US-09-465-901-12	Sequence 12, Appl
3	13	4.1	223	4	US-09-465-901-26	Sequence 26, Appl
4	13	4.1	223	4	US-09-465-901-46	Sequence 46, Appl
5	13	4.1	286	1	US-08-118-270-65	Sequence 65, Appl
6	13	4.1	286	5	PCT-US93-08528-65	Sequence 65, Appl
7	13	4.1	316	2	US-08-827-291A-2	Sequence 2, Appli
8	12	3.8	293	1	US-08-118-270-60	Sequence 60, Appl
9	12	3.8	293	5	PCT-US93-08528-60	Sequence 60, Appl
10	12	3.8	333	3	US-08-988-876-6	Sequence 6, Appli
11	11	3.5	222	2	US-08-467-948A-27	Sequence 27, Appl
12	11	3.5	222	3	US-08-467-947A-27	Sequence 27, Appl
13	11	3.5	224	4	US-09-465-901-30	Sequence 30, Appl
14	11	3.5	284	1	US-08-118-270-61	Sequence 61, Appl
15	11	3.5	284	5	PCT-US93-08528-61	Sequence 61, Appl
16	11	3.5	296	2	US-08-467-948A-2	Sequence 2, Appli
17	11	3.5	296	3	US-08-467-947A-2	Sequence 2, Appli
18	10	3.2	223	4	US-09-465-901-14	Sequence 14, Appl
19	10	3.2	223	4	US-09-465-901-16	Sequence 16, Appl
20	10	3.2	223	4	US-09-465-901-20	Sequence 20, Appl
21	10	3.2	223	4	US-09-465-901-24	Sequence 24, Appl
22	10	3.2	223	4	US-09-465-901-28	Sequence 28, Appl
23	10	3.2	223	4	US-09-465-901-32	Sequence 32, Appl
24	10	3.2	223	4	US-09-465-901-36	Sequence 36, Appl
25	10	3.2	223	4	US-09-465-901-40	Sequence 40, Appl
26	10	3.2	223	4	US-09-465-901-42	Sequence 42, Appl
27	10	3.2	247	1	US-08-465-980-3	Sequence 3, Appli
28	10	3.2	247	2	US-09-053-303-3	Sequence 3, Appli
29	10	3.2	247	4	US-09-339-115-3	Sequence 3, Appli
30	10	3.2	247	5	PCT-US95-07093-3	Sequence 3, Appli
31	10	3.2	269	1	US-08-118-270-64	Sequence 64, Appl
32	10	3.2	269	5	PCT-US93-08528-64	Sequence 64, Appl
33	10	3.2	274	1	US-08-118-270-69	Sequence 69, Appl
34	10	3.2	274	5	PCT-US93-08528-69	Sequence 69, Appl
35	10	3.2	275	1	US-08-118-270-66	Sequence 66, Appl
36	10	3.2	275	5	PCT-US93-08528-66	Sequence 66, Appl
37	10	3.2	277	1	US-08-118-270-68	Sequence 68, Appl
38	10	3.2	277	5	PCT-US93-08528-68	Sequence 68, Appl
39	10	3.2	284	1	US-08-118-270-67	Sequence 67, Appl
40	10	3.2	284	5	PCT-US93-08528-67	Sequence 67, Appl
41	10	3.2	314	3	US-08-988-876-7	Sequence 7, Appli
42	10	3.2	320	1	US-08-465-980-2	Sequence 2, Appli
43	10	3.2	320	2	US-09-053-303-2	Sequence 2, Appli
44	10	3.2	320	4	US-09-439-313-527	Sequence 527, App
45	10	3.2	320	4	US-09-339-115-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-465-901-44
; Sequence 44, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expession Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-44

Query Match 4.1%; Score 13; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 MAYDRYVAICHPL 130
||||||||||||
Db 55 MAYDRYVAICHPL 67

RESULT 2
US-09-465-901-12
; Sequence 12, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expession Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57

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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 223
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: PCR primer
US-09-465-901-12

  Query Match             4.1%;  Score 13;  DB 4;  Length 223;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db         55 MAYDRYVAICHPL 67


RESULT 3
US-09-465-901-26
; Sequence 26, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
;  APPLICANT: Reed, Randall
;  APPLICANT:  Yau, King-Wai
;  APPLICANT:  Krautwurst, Dietmar
;  TITLE OF INVENTION: Olfactory Receptor Expession Libraries
;  TITLE OF INVENTION:  ad Methods of Making and Using Them
;  FILE REFERENCE: 001107.00105
;  CURRENT APPLICATION NUMBER: US/09/465,901
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 60/112,605
;  PRIOR FILING DATE: 1998-12-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 223
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: PCR primer
US-09-465-901-26

  Query Match             4.1%;  Score 13;  DB 4;  Length 223;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db         55 MAYDRYVAICHPL 67


RESULT 4
US-09-465-901-46
; Sequence 46, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
;  APPLICANT: Reed, Randall
;  APPLICANT:  Yau, King-Wai
;  APPLICANT:  Krautwurst, Dietmar
;  TITLE OF INVENTION: Olfactory Receptor Expession Libraries
;  TITLE OF INVENTION:  ad Methods of Making and Using Them
;  FILE REFERENCE: 001107.00105
;  CURRENT APPLICATION NUMBER: US/09/465,901
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 60/112,605
;  PRIOR FILING DATE: 1998-12-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH: 223
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: PCR primer
US-09-465-901-46

  Query Match             4.1%;  Score 13;  DB 4;  Length 223;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db         55 MAYDRYVAICHPL 67


RESULT 5
US-08-118-270-65
; Sequence 65, Application US/08118270
; Patent No. 5508384
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Randall B.
;    APPLICANT:  Schuster, David I.
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,270
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  286 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-118-270-65

  Query Match             4.1%;  Score 13;  DB 1;  Length 286;
  Best Local Similarity   100.0%;  Pred. No. 0.0004;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db         92 MAYDRYVAICHPL 104


RESULT 6
PCT-US93-08528-65
; Sequence 65, Application PC/TUS9308528
;  GENERAL INFORMATION:
;    APPLICANT:  New York University
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
```

```
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08528
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  286 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08528-65

  Query Match             4.1%;  Score 13;  DB 5;  Length 286;
  Best Local Similarity   100.0%;  Pred. No. 0.0004;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHPL 130
              |||||||||||||
Db         92 MAYDRYVAICHPL 104


RESULT 7
US-08-827-291A-2
; Sequence 2, Application US/08827291A
; Patent No. 5874243
;  GENERAL INFORMATION:
;    APPLICANT:  Macina, Roberto
;    APPLICANT:  Sathe, Ganesh
;    TITLE OF INVENTION:  NOVEL OLRCC15 RECEPTOR
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/827,291A
;      FILING DATE:  28-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  King, William T
;      REGISTRATION NUMBER:  30,954
;      REFERENCE/DOCKET NUMBER:  GP50001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5015
;      TELEFAX:  610-270-5090
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  316 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-827-291A-2

  Query Match             4.1%;  Score 13;  DB 2;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        285 LNPLIYSLRNKEV 297
              |||||||||||||
Db        285 LNPLIYSLRNKEV 297


RESULT 8
US-08-118-270-60
; Sequence 60, Application US/08118270
; Patent No. 5508384
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Randall B.
;    APPLICANT:  Schuster, David I.
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,270
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  293 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-118-270-60

  Query Match             3.8%;  Score 12;  DB 1;  Length 293;
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  Best Local Similarity   100.0%;  Pred. No. 0.0035;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHP 129
              ||||||||||||
Db         90 MAYDRYVAICHP 101


RESULT 9
PCT-US93-08528-60
; Sequence 60, Application PC/TUS9308528
;  GENERAL INFORMATION:
;    APPLICANT:  New York University
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08528
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  293 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08528-60

  Query Match             3.8%;  Score 12;  DB 5;  Length 293;
  Best Local Similarity   100.0%;  Pred. No. 0.0035;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHP 129
              ||||||||||||
Db         90 MAYDRYVAICHP 101


RESULT 10
US-08-988-876-6
; Sequence 6, Application US/08988876
; Patent No. 6063596
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Yue, Henry
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTORS ASSOCIATED
;    TITLE OF INVENTION:  WITH IMMUNE RESPONSE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,876
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0441 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  333 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  205814
US-08-988-876-6

  Query Match             3.8%;  Score 12;  DB 3;  Length 333;
  Best Local Similarity   100.0%;  Pred. No. 0.0039;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        118 MAYDRYVAICHP 129
              ||||||||||||
Db        118 MAYDRYVAICHP 129


RESULT 11
US-08-467-948A-27
; Sequence 27, Application US/08467948A
; Patent No. 5998164
;  GENERAL INFORMATION:
;    APPLICANT:  LI, YI
;    APPLICANT:  CAO, LIANG
;    APPLICANT:  NI, JIAN
;    APPLICANT:  GENTZ, REINER
;    APPLICANT:  BULT, CAROL J.
;    APPLICANT:  SUTTON III, GRANGER G.
;    APPLICANT:  ROSEN, CRAIG A.
;    TITLE OF INVENTION:  Polynucleotides Encoding Human G-Protein
;    TITLE OF INVENTION:  Coupled Receptor GPR2
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PATENTIN RELEASE #1.0, VERSION #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,948A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04079
;      FILING DATE:  30-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFE, ERIC K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.1140003/EKS/KLM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  222 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
US-08-467-948A-27

  Query Match             3.5%;  Score 11;  DB 2;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 YDRYVAICHPL 130
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Db         60 YDRYVAICHPL 70


RESULT 12
US-08-467-947A-27
; Sequence 27, Application US/08467947A
; Patent No. 6090575
;  GENERAL INFORMATION:
;    APPLICANT:  LI, YI
;    APPLICANT:  CAO, LIANG
;    APPLICANT:  NI, JIAN
;    APPLICANT:  GENTZ, REINER
;    APPLICANT:  BULT, CAROL J.
;    APPLICANT:  SUTTON III, GRANGER G.
;    APPLICANT:  ROSEN, CRAIG A.
;    TITLE OF INVENTION:  Polynucleotides Encoding Human G-Protein
;    TITLE OF INVENTION:  Coupled Receptor GPR1
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PATENTIN RELEASE #1.0, VERSION #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,947A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04079
;      FILING DATE:  30-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFE, ERIC K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.1140002/EKS/KLM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  222 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
US-08-467-947A-27

  Query Match             3.5%;  Score 11;  DB 3;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 YDRYVAICHPL 130
              ||||||||||| 
Db         60 YDRYVAICHPL 70


RESULT 13
US-09-465-901-30
; Sequence 30, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
;  APPLICANT: Reed, Randall
;  APPLICANT:  Yau, King-Wai
;  APPLICANT:  Krautwurst, Dietmar
;  TITLE OF INVENTION: Olfactory Receptor Expession Libraries
;  TITLE OF INVENTION:  ad Methods of Making and Using Them
;  FILE REFERENCE: 001107.00105
;  CURRENT APPLICATION NUMBER: US/09/465,901
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 60/112,605
;  PRIOR FILING DATE: 1998-12-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;    LENGTH: 224
;    TYPE: PRT
;    ORGANISM: Mus musculus
;    FEATURE:
;    OTHER INFORMATION: PCR primer
US-09-465-901-30

  Query Match             3.5%;  Score 11;  DB 4;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 YDRYVAICHPL 130
              ||||||||||| 
Db         57 YDRYVAICHPL 67


RESULT 14
US-08-118-270-61
; Sequence 61, Application US/08118270
; Patent No. 5508384
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Randall B.
;    APPLICANT:  Schuster, David I.
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,270
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  284 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-118-270-61

  Query Match             3.5%;  Score 11;  DB 1;  Length 284;
  Best Local Similarity   100.0%;  Pred. No. 0.029;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 YDRYVAICHPL 130
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Db         95 YDRYVAICHPL 105


RESULT 15
PCT-US93-08528-61
; Sequence 61, Application PC/TUS9308528
;  GENERAL INFORMATION:
;    APPLICANT:  New York University
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08528
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  284 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08528-61

  Query Match             3.5%;  Score 11;  DB 5;  Length 284;
  Best Local Similarity   100.0%;  Pred. No. 0.029;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 YDRYVAICHPL 130
              ||||||||||
Db         95 YDRYVAICHPL 105


Search completed:  October  5, 2004, 14:25:40
Job time :  42 secs
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